

QY 512 NDMIGLPEPLATIGEDVSGMPTVCIPEDDGEVDGRLHMAVADKWEIIQRDEDKM 571  
I : : : I : : : I : : : I : : : I : : : I : : : I : : : I : : :  
Db 471 NSVAVSYFPGILISTADEESTSMWPMVPTRYVGLGKNLK-----NMN 511

QY 572 G---DIIVMLTNRRLMEKCVSVAESHDQALVGDKTIAFWLMDKMYIDFMALDRPSTPLID 628  
I : : : I : : : I : : : I : : : I : : : I : : : I : : : I : : :  
Db 512 GWMHMDLDYFSMDPV-----FRGHNSI-----TFSMWNHSENY-MLALSHDE----- 555

QY 629 RGVALKHKIRLLITNLGGE--GYLN-----FMGNEGH--FEWLDFPRG 668  
I : : : I : : : I : : : I : : : I : : : I : : : I : : : I : : :  
Db 556 ---VVHGKSNMGKMPGDGWOKYAVRALFTYMTHHPGKRITFMEMERGEQMSWWV--G 610

QY 669 DLHLPSKGFPVPNNYSYDKCRRRRFLDLSNKLRYHGMOEFDQAIOHLE-----AYGFM 722  
I : : : I : : : I : : : I : : : I : : : I : : : I : : : I : : :  
Db 611 DLEMILLNPP-----HOOLKOFTELHMLTKNEPALYSNDPD 648

QY 723 TSEHOYSRKDERDIRIIFVERGN-----LVFVFNFHWTSYSDYRVQCLKPGRKYIYLD 776  
I : : : I : : : I : : : I : : : I : : : I : : : I : : : I : : :  
Db 649 ESGFGIMCSDNRHSVSPRIIRAKNSAEFYVYICNF-FQHPSHYRGVPGPYGFTELFEN 707

QY 777 SDDPLEFGG--GGRLSHD-AEHFSEGWDNRPKRSTMYVTTPCTATVYALVEDEVEN 829  
I : : : I : : : I : : : I : : : I : : : I : : : I : : : I : : :  
Db 708 SDARQYGSGSNMGKLGCKWTWEWSFH----EQPYSLDLCLPPLISVLVKLSQAAEEN 759

RESULT 8  
GLGB\_BACST STANDARD: PRT: 639 AA.

ID GLGB\_BACST STANDARD: PRT: 639 AA.  
AC P30538;  
DT 01-APR-1993 (Rel. 25, created)  
DT 01-APR-1993 (Rel. 25, last sequence update)  
DT 01-FEB-1995 (Rel. 31, last annotation update)  
DE 1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) (GLYOGEN BRANCHING ENZYME).  
GN GLGB.  
OS Bacillus stearothermophilus.  
OC Bacteria; Firmicutes; Bacillales/Clostridium group;  
OC Bacteria/Staphylococcus group; Bacillus.  
OX NCBI\_TaxID=14422;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=1503-4R;  
RX MEDLINE=92079888; PubMed=1745226;  
RA Kiel J.A.K.W., Boels J.M., Beidman G., Venema G.;  
RT "Molecular cloning and nucleotide sequence of the glycogen branching enzyme gene (glgB) from Bacillus stearothermophilus and expression in Escherichia coli and Bacillus subtilis.";  
RT Mol. Gen. Genet. 230:136-144(1991).  
RL M.O. gen. Genet. 230:136-144(1991).  
CC -1- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF GLYOGEN.  
CC -1- PATHWAY: THIRD STEP IN GLYOGEN BIOSYNTHESIS.  
CC -1- MISCELLANEOUS: THE TEMPERATURE FOR OPTIMAL ACTIVITY IS APPROXIMATELY 55 DEGREES CELSIUS.  
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.  
CC -----  
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CC CC  
Cc EMBL: M35089: AAA22482.1; -.  
DR PIR: S18599; S18599.  
DR InterPro: IPRO00461; -.  
DR Pfam: PF00128; alpha-amylase; 1.  
KW Glycogen biosynthesis; Transferase; Glycosyltransferase.  
FT ACCT SITE 309 309 BY SIMILARITY.  
FT ACCT SITE 352 352 BY SIMILARITY.  
FT ACCT SITE 420 420 BY SIMILARITY.  
SQ SEQUENCE 639 AA: 74795 MW: F5BD4446B371E03A CRC64;

	Query Match Similarity	12.6%:	Score 572;	DB 1:	Length 639;	
	Best Local Similarity	26.0%:	Pred No.6,le-34:			
	Matches 184;	Conservative 109;	Mismatches 232;	Indels 182;	Gaps 28;	
QY	177 YEGSLDAFSGRYEKTGF----	SRETGITYREMARCATWAALIGDFNMNN--PNADVMTON	231			
DB	15 HBSGLT---KYSELGCANHYKKNMGWTFRCVAPAHAREVLRLVGSSFNENNGTNFMNKKVS	71				
QY	232 ECGWVEFLPNNADGSPPRIPHGRXKIRMDTPSSGN--KSIP-----AMTKESV	278				
DB	72 NCGWMMIFLPEMLE-----GHLYKEITTYDGNVLKSDYAFYSILRPHASTASIVNI	124				
QY	279 QAGELPYNGIYIDDPREEEKUYFKNPQRPRKSLRIYESHVG--MSSTEPVINTYANFRD	336				
DB	125 KG---YQMNDQWRKKRKOKKRRTYDQP-----LFETIELHFGSMWKKEGDSYYTYOEMAE	174				
QY	337 DYLPRIKLGIYNAVOLMAIOESHYYAASEGYHTVNTNYTAASSRGTPDDLSLKDKANEGL	396				
DB	175 EIIPIYLLEHGFIHEILLRPVEHPFDOSMGOIGYASATSRGTPTDLMLYFTDRCHQAGI	234				
QY	397 LVLMIDVSHASTNTLDGLNMFPGDTGHNFGHSGRPCRHNMCMPSRLFNYSWEVLERFLSN	456				
DB	235 GYILDMVPBHFCKDS--HGLYMFDGARAYLEYAMODREANTYWGSTANFDLGPREVRSLISN	293				
QY	457 ARMWLDYEKFEDGFREDGVTSMMYTTHGLIOVDTEGYNEXFYGAUVDAAVYLLMLDMITH	516				
DB	294 ALFWMEYFHVDGFBDVAVALMYLWPNS--DVLYKNFY-----AVEFLQKLNFTVF	341				
QY	517 GLFPREAVTIAGEDVSGMPRTYCIEVEDGGVGFEDRYRNAVAADKVVETIQKDEDMKMGDLYH	576				
DB	342 AYDPNLTMLIAESTDMPRTAPTARYDGGLSEFNK-----WNKGMMND	382				
QY	577 MTL-----NRWMLEKCV-----SYAE-----SHDQALVGDKTIAHWLMDKXDUTDEM	617				
DB	383 ILTYMETPREBHKKYVNKKYTFSLYLAWSNFLPERHSEDVHVGKSL-----	429				
QY	618 ALDRSTPLIDRGVALHKM-----IRLTIMGISEGY-----LPMNGNEBH	659				
DB	430 -----LSKMPGYEEKFAQLRL-----YGyllTHPGKLLLFMGGEFGQ	468				
QY	660 --RWIMDFPRGDDLHPGSKGVLPNGNYSYDKCRRRPDLGNSKHL-----RYHGMQEF	708				
DB	469 FBEKWDLEDLDML-----FD-----FDMHRMMNTYVELLKCYRKRYPLYEL	511				
QY	709 DOAIOHLE--EAAYGEMTSEHOYISRKDERBRILIIVERGNLVLFVNFHMWTSSYSDYRVGCL	766				
DB	512 DHPSPDGFIEWIDVNAEQSIFSIFIRGKKEDDL-----LIYVCNE--TKVYHGYKVGPV	563				
QY	767 KKGKXYIVDDSDPLFGGGRSLSHAENHSFEGWYXNRRSPVYTR	813				
DB	564 LFTRYREVINSDAOIGGFGGNI--NPKRIAMGSPRFKHYPHIOTMTP	609				
RESULT 9						
GLGB_ECOLI						
ID	GLGB_ECOLI	STANDARD:	PRT:	728 AA.		
AC	P07762:					
DT	01-AUG-1988 (Rel. 08, Created)					
DT	01-AUG-1988 (Rel. 08, Last sequence update)					
DT	01-NOV-1997 (Rel. 35, Last annotation update)					
DE	1,4-ALPHA-D-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) (GLYCOGEN BRANCHING ENZYME).					
GN	GLGB.					
OS	Escherichia coli.					
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;					
OC	Escherichia.					
OX	NCBI_TaxID=562;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=86250792; PubMed=3013861;					
RA	Baecker P.A., Greenberg E., Pleiss J.;					

"Biosynthesis of bacterial glycosylated primary structure of Escherichia coli 1,4-alpha-D-glucan:1,4-alpha-D-glucan 6-alpha-D-(1,4-alpha-D-glucan)-transferase as deduced from the nucleotide sequence of the glgB gene."

RT J. Biol. Chem. 261:8738-8743(1986).

RA SEQUENCE FROM N.A.  
RA STRAIN-K12 / MG1655.  
RA BLATNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V., RILEY J., COLLADO-VIDES J., GLASNER J.D., RODE C.K., MAYHEW G.F., GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J., MAU B., SHAO Y.  
RA "The complete genome sequence of Escherichia coli K-12."  
RT Science 277:1453-1474(1997).

CC -1 CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF GLYCOSYL.  
CC -1 PATHWAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS.  
CC -1 SUBUNIT: MONOMER.  
CC -1 SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.

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CC EMBL: M13751; AAA2872.1; -  
DR EMBL: U16897; AAA38230.1; -  
DR EMBL: AE000419; AAC76457.1; -  
DR PIR: A25498; NDECA.  
DR Ecogen: EG10378; glgB.  
DR InterPro: IPR000461; -  
DR Pfam: PF00128; alpha-amylase, 1.  
KW Glycosyltransferase; transferase; Glycosyltransferase.  
FT ACT\_SITE 405 405 BY SIMILARITY.  
FT ACT\_SITE 458 458 BY SIMILARITY.  
FT ACT\_SITE 526 526 BY SIMILARITY.  
SQ SEQUENCE 728 AA; 84336 MW; 0F20AF367BF2015 CRC64;

Query Match 12.6%; Score 571.5; DB 1; Length 728;  
Best Local Similarity 25.4%; Pred. No. 8.1e-34;  
Matches 205; Conservative 110; Mismatches 276; Indels 217; Gaps 32;

OY 105 MDDIVEDEVRK-----ESVPRREYISIRKISKPSRIPP-----PGRGOR 145  
DB 1 MSDRIDRVITALAGHPADPFSVLGMHKTAA-----GLEVRALLPDTDWVLEPKTRK 56  
OY 146 IYDD-PSLGE-----RQHLDRYS-----QYKRLREIDIKYESLD 182  
DB 57 LAKLECLDSRFSGVPRKRNFRITQLAVWVHCOQLIDPVEFGPLIDMDMLLSEG 116  
OY 183 AFSNGYEFGFSRSE-----IGITRENAFGATWALIGDFNNMNPNDVW-TONEGCVWE 237  
DB 117 THLPRTYELGHAADTMDGVTGTRSVAPNARVSVVGQFYMVGRRHPMLRRESIME 176  
OY 238 IFLENNADGSPPIPHSGRVKIRMDTPSGKNDISPAWIKFSVQAGE-----LPYNGIY 290  
DB 177 LFIRG-----AHNGOLYKXEMIDANGNLRKSDPYAFEMOMPEVASILGIPKVV- 228  
OY 291 YDPEEEKYVKNPQPKRPSLRITYESHVGSSTPEYINTYANR-----DVLPRIKLGY 347  
DB 229 --QTEERKKAQOFDAP-----ISIEVHLCSWRHRTDNNEFWLSYRELADQVPAKMGF 281  
OY 348 NAOVLMAIOESYASYAFGYHTNTFYAASSRGPPDDLSKLDKAKHELGVLVINDIYSHA 407  
DB 282 THEELPLINHEPFGSMGVOPTGLVAPTRGRTDDEPRYFIDAHAGNAGLVIIIDWVGHF 341  
OY 408 STNLDLQNLNMFDTGDGHTYFHSGR-GHMMWMDSKLFYNGSWEVYLRFLLSNARWMDYKRF 466

DB 342 PTUDDF-ALAEFGDTN-LYHSDPRECYHODWNTLTYNRRREVSFLYNALMYLIRRCI 399  
OY 467 DGRFPGVTSNMTTHHGLOVDFTGNNEY-----FGATVDVAVVYLMMLNDMIRIGLPEEA 522  
DB 400 DALRVAVASMYR-----DYSRKEGEMIPNDFGRENLEALFRLNTRNLGLGVSGA 453  
OY 523 VTIGEDVSGMPYVCPVEDGCVGFDRRLHMAVADKWEITQKRDEMKMGDIYHM/TNR 582  
DB 454 VYMAESTDFPGVSRPDQMGGLGFYWK-----WNLG----- 484  
OY 583 WLEKCVSYAE-----SHDQALVGDKTIAFWLIDKDM 613  
DB 485 WMHDTLDYMKRLPVRYROYHNDKLTGILYNTYENFLPSHDEYVHGKRSI----- 535  
OY 614 YDFMALDRSTPLIDRGVALHKMIRLITWGLGEGY-----INFMGNERFH-PE 661  
DB 536 ----LDPRP-----GDAMOKFANL-----RAYGWMMAFPKGLLFMGNEFVQGR 577  
OY 662 WIDPRGDIHLPSGKRVPCNNYSYDCKRRRPLDGSNKHRLRYHGMOPFOAIOHLEAYGF 721  
DB 578 WNHDAFLDWHLEGG-----GDMNHGQRLVRLD-NITYRHHKAMELD-----FDPYGF 626  
OY 722 MISEHOYISRKDERDILYFER-----GNLYFVENFHTSYSDYVSGLKPSGKYK:YIDS 777  
DB 627 ----EMLYVDKREKSVLLFVRDRKGNELIYASNTFVPRRDYDFGGINOPKMWJLINT 681  
OY 778 DDFLEGGFGR-----LSHDAEH 794  
DB 682 DSMHYHSNANGNGVYHSDPIASHGRQH 709

RESULT 10  
GLOB\_HAEIN STANDARD: PRT; 730 AA.  
ID GLOB\_HAEIN  
AC P45177;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE 1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) (GLYCOGEN BRANCHING ENZYME).  
GN GLOB OR H11357.  
OS Haemophilus influenzae.  
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
OC Haemophilus.  
OX NCBI\_Taxid=727;  
RN [1]  
RP SEQUENCE FROM N.A.  
RP STRAIN-RD / KM20 / ATCC 51907;  
RX MEDLINE=95350630; PubMed=7542800;  
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Sulten G., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shiley R., Liu L.-I., Glodde A., Kelley J.M., Weidman J.F., Phillips C.A., Sprague D., Hedblom E., Cotton H.D., Uettermann T.R., Hanna M.C., Nguyen D.T., Sadek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fritchman J.L., Geoghegan N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;  
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";  
RT Science 269:496-512(1995).  
CC -1 CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF GLYCOSYL.  
CC -1 PATHWAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS.  
CC -1 SUBUNIT: MONOMER (BY SIMILARITY).  
CC -1 SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.

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CC -----  
 DR EMBL: U32815; AAC23004.1; -  
 DR TIGR: H11357; -  
 DR InterPro: IPR000461; -  
 DR Pfam: PF00128; alpha-amylose; 1.  
 KW Glycogen biosynthesis; Transferase; Glycosyltransferase.  
 FT ACT\_SITE 405 405 BY SIMILARITY.  
 FT ACT\_SITE 458 458 BY SIMILARITY.  
 FT ACT\_SITE 526 526 BY SIMILARITY.  
 SQ SEQUENCE 730 AA; 83820 MW; 5B9575317F53/69A CRC64;

Query Match 12.5%; Score 566; DB 1; Length 730;  
 Best Local Similarity 24.9%; Pred. No. 2e-33; Indels 198; Gaps 38;  
 Matches 209; Conservative 139; Mismatches 295;

QY 61 MVAASKRVLPDGRICYSSTDLAAGTVSESOVLIVDSLIMDK--IVEDEVNKE 117  
 D 1 MTTAVQAIIIDGFPD--ASNGDPFALGMHETDGT--ELRTLLPANRVVIERESGKE 56  
 QY 118 SVPRFETVSTIRK--IGSKPRSIIPPGHGRITYIDSLGFRGHLDRISQYRLKEID 175  
 D 57 ITTEL-DCVDERGFEVVG----VIPNCKOPFAYOLOVFWGNEAOIIDPY-RFHPMIDDLE 109  
 QY 176 KYBSGLDAFSGYKEKGFSE--TGIRREMAPCATMAALIGFNNMNPADVMT-Q 230  
 D 110 QWLISSESMRLPEYVLGAHMECDGVSQVNFRLMAPARVSTVGDNPWDGRHPRH 169  
 QY 231 NECGWEIPLPNADG-----SPPIPHGRVYKIRNDTPSGNKDSIPAW 273  
 D 170 SKGSWMLFLPKASLGQLYKFLIDCHGNLRKADPPAFSS--QLRDTAS-QVSLAPNV 226  
 QY 274 IKSVAQAGELPYNGIYDDPEEKYVFNKPPKPSLRITYSHVGMSTEVIN---T 330  
 D 227 VEMT-----EARKKANOONP-----ISIEVHGLGSMRNLNNEMWLD 264  
 QY 331 YANRDVULRIKRLGNVAVOLAMIOHSYASFGYVHTFVAASSFGPDCLKSLIDK 390  
 D 265 YDQIADDELIPYKEMGTHLEPLSEPPDGSWGTOPDLISYTSRFGSEFRLVKR 324  
 QY 391 AHEGLILVMDIYHSAHSTWTLGLNMFDSGDHGFHSGPR-GHHMMWDSRLFNYSWEV 449  
 D 325 AHEGLIVIIIDWVGRHPSPT-HGLVAFDGT-ALYEHEDPREGHQWMTLIYVNGREV 382  
 QY 450 LRFILSNARWLDKFKDGRFRFGVTSMTTHGLQVDFGNNEY----FGATIDVAV 505  
 D 383 KNFLSSNALYWLERFGVDGIRVAVASMIYR-----DYSRAEGEWIPNOYGGRENLEAI 436  
 QY 506 VYIALLMDMIHGLPEAVTIGEDVSGMPYVCIPEVDGVSFEDYRLHMAVADKWEIIQKR 565  
 D 437 EFLKHTMKIKHSEMAAGLSTAEESTFAGYTHPSENGGLGFNPKMNNG----- 484  
 QY 566 DEDWKMDIYHMLT-----NRWLKCVSYAE-----SHDQ-----ALVGDXTI 604  
 D 485 ---WMNDTLAVMKIDPIYRQYHNKMTFGMYQYSENFVLLSHDEYVHKGYSILKMPG 541  
 QY 605 AFWLMDDM---YDFMLDRSTPLIDRGVALHMKIRLITMGSGEGLYLFPMGSEGH-P 660  
 D 542 DTWQKFAFLRAYGYM-----WGYPGKLL-FMGNEFQGR 576  
 QY 661 EM-----IDPRGLHLPSC-----KFVPGNNYSYDKCRFRPDLGSKHLRYHGMQEPD 709  
 D 577 EMNTEESIDWLDLDBENIGGHHKVLKLVKDNOIYOKNRLPELDNSPE----- 626  
 QY 710 QAIOHLEAVGEFMTSEHQYISRKDERDRIIVERGN-----LVEFNFHMTSISDYRVG 764  
 D 627 -----GF-----DWLVDDAANSVLAFFERRSNGERIIVYVSFTVPRH-NYRIG 670  
 QY 765 CLKRGKTIYVDSDDPLF-----GGFRLSHDAHFSEGVYDNRPRSPFWYPCRTAVY 819  
 D 765 CLKRGKTIYVDSDDPLF-----GGFRLSHDAHFSEGVYDNRPRSPFWYPCRTAVY 819

DB 671 VNVACKYEELIANTDSMTYEGSNVGNFCGYA--SEQIESH-----RENSISVIP-PLATV 723  
 QY 820 Y 820  
 DB 724 Y 724

RESULT 11  
 ID GLGB\_AGRU STANDARD; PRT; 734 AA.  
 AC P52979;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE 1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) (GLYCOGEN BRANCHING  
 DE ENZYME).  
 GN GLGB.  
 OS Agrobacterium tumefaciens.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Agrobacterium.  
 OX NCBI\_TaxID=362;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A348;  
 RC MEDLINE=99069330; PubMed=9851999;  
 RA Ugalde J.E., Lepek V., Uttaro A.D., Estrella J., Iglesias A.,  
 RA Ugalde R.A.;  
 RT "Gene organization and transcription analysis of the Agrobacterium  
 RT tumefaciens glycogen (glg) operon: two transcripts for the single  
 RT phosphoglucomutase gene."  
 RL J. Bacteriol. 180:6557-6564 (1998).  
 CC -1- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF  
 CC GLYCOGEN.  
 CC -1- PATHWAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOGLYD HYDROLASES. ALSO  
 CC KNOWN AS THE ALPHA-AMYLASE FAMILY.  
 CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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DR EMBL: AF03856; AAD03472.1; -

DR InterPro: IPR000461; -

DR Pfam: PF00128; alpha-amylose; 1.

KW Glycogen biosynthesis; Transferase; Glycosyltransferase.

FT ACT\_SITE 417 417 BY SIMILARITY.

FT ACT\_SITE 470 470 BY SIMILARITY.

FT ACT\_SITE 538 538 BY SIMILARITY.

SQ SEQUENCE 734 AA; 83623 MW; 70A3CD35A7F31E6 CRC64;

Query Match 11.9%; Score 542.5; DB 1; Length 734;  
 Best Local Similarity 23.8%; Pred. No. 1e-31;  
 Matches 182; Conservative 123; Mismatches 266; Indels 193; Gaps 32;

QY 119 VPRMRETVSTIRKSGKRSIPPGRGRIYDIPDSLTG-----FRQHLDRYSQ-- 166  
 D 36 IPLHETPE-----GFSARCFIPGAEEVSVLTGONFVGLKQIDPDGFFGRIDLSKROPV 91  
 QY 167 -YKRLREE-----IDKY-----EGSLDAFSGYKEKFGFS-RSETGITYRE 204  
 D 92 RYRACDDADEMAVATDPSYSGVLPAMDYFVREGSICGSGTGMARPLKLEGVGFHFAV 151  
 QY 205 WAPGATMAALIGDENNNMNPADVMT-QNECGWEIPLPN-----NADGS-PPL- 250  
 D 152 WAPNGRVSAYVGFNNMWDRRHMYRFRKDTGIMEIFADPVYACAYKFEILGANGELPLK 211  
 QY 251 --PHGRVIVIRNDTPSGNNDSPAWIKFSVQAPGELPYNGIYDDPEEKYVFNKPPK 308

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Db 212 ADPARRRELAPKNA-----SYTAP-ELTOK--WEOAHREHNA---QVDR 252
Cc 309 PKSLRYESHNG--MSSEPIYNTYANFRDVIYPRIKKLYANAVOLAIQESHYASFGY 366
Cc 253 RQPSITIEVHAGSMQSBGDFGLSDELEAOLITCTDGMGTHTHEFTIEHPIDPSWGY 312
Cc 367 HTVTFYAAASFRTDPLKSLIDKAHELGLVLMIDYHSHASTVTLQDLMFDTGCHYF 426
Cc 313 OTTGATATARKGDEGPARFVNSAHKVGIGVLDWPAHPIDE--HGLWFOET-ALYE 370
Cc 427 HSGFR-GHHMMWDSRLFNYSGWELREFLLSNARWMLDEYKDFGFRDGYTSMYTHHGLQ 485
Cc 371 HADPRGHPDMNTAIXNFGRIEYMSYLINNALYMAERFHLGLRVAVASMLY----- 424
Cc 486 VDETGNNEY---FGYATDVAVVYLMILNDMIGLFEPAVITIGEDVSGMPTVCIPEVD 541
Cc 425 LDYRKRGEWYIPNEYGRENLESYRFLQKNMSLYVGTNPGVMTJAEESTSMKPYSGVHE 484
Cc 542 GGVEFDYRLHMAVADKWEIIOKRDEDMKMG-----DIVHMLTNRRLKCVSY 590
Cc 485 GGLGFGFK-----WNMGFMHDTLSYFSREPVHRKFFHOELTEGLY 525
Cc 591 A-----ESHQDALVGDKTIAFWLMDKMDYDMALDRSTPLIDRGVALHKMIRLITM 642
Cc 526 AFTEFNFLPSHDEIVHKGKSLIAKMSGDDMOKPAFL-----RSYGFMM 570
Cc 643 GLGEGYLNFGNFEFGH-PEWIDPRGDLHPSGKFVPGNNYSYDKORRRFDLGNKHLR 701
Cc 571 GYPRKTL-FMGQEFAGMSEMS--KQSL-----DMNLR 601
Cc 702 YHNGOE-FDQALQLEAAGXGEMSEHOXISKRDERDRIYFERGNLVFVNFHW----- 754
Cc 602 QYRHEGMRKLYRDLNTYTSKALHARCDERDFRMLVVDHNSVFA---WLRTAPG 657
Cc 755 -----TSSY-SDYRVGCLAPKRYKYIVLSDDPLEFGFGR 787
Cc 658 EKPAVAVICNLPYRENYVPLVAGRWIRLINDAETIGSGK 701

RESULT 12
GLGB_BACCL STANDARD: PRT: 666 AA.
AC P30537;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE 1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) (GLYCOGEN BRANCHING ENZYME).
GN GLGB.
OS Bacillus caldolyticus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
CX NCBI_TaxID-1394;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-93208370; PubMed-1296817;
RA Kiet J.A.K.W., Boels J.M., Belman G., Venema G.;
RT "The glbB gene from the thermophile Bacillus caldolyticus encodes a thermostable branching enzyme.";
RL DNA Seq. 3:221-232(1992).
CC -1- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF GLYCOGEN.
CC -1- PATHWAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS.
CC -1- MISCELLANEOUS: OPTIMAL ACTIVITY AT APPROXIMATELY 39 DEGREES CELSIUS.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
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Cc -----
Cc DR EMBL: 214057; CAA/8440.1; -.
Cc DR InterPro: IPR000461; -.
Cc DR Pfam: PF00128; alpha-amylase; 1.
Cc KW Glycogen biosynthesis; transferase; glycosyltransferase.
Cc FT ACT_SITE 309 309 BY SIMILARITY.
Cc FT ACT_SITE 352 352 BY SIMILARITY.
Cc FT ACT_SITE 420 420 BY SIMILARITY.
Cc SQ SEQUENCE 666 AA; 78096 MW; 1F64C31495B1B6E CRC64;

Query Match 11.9%; Score 539.5; DB 1; Length 666;
Best Local Similarity 26.9%; Pred. No. 1.5e-31;
Matches 181; Conservative 93; Mismatches 238; Indels 161; Gaps 26;

Cc 177 YEGSLDAFSGYKFGF-----SRSEGITYREMAPGATMAALIGDFNMNM--PNADVTQN 231
Cc 15 HEGRL---YQSEYELGAVIRGGAVGTRFCVMAHAEVRLVGSFNQNTNSPTKVN 71
Cc 232 ECGWEIPLPNNAGS---PIPHSGRYKIMDPDPSGNKSIPIAWKFSVQAGELPYN 287
Cc 72 DSGVTVIVPEMLGHLKYEITTPDGRVLLKADPAYSLELPHASIVYDLKG--YENN 130
Cc 288 GIYDPREEKYVFNPKPKRSKSLRIYESHVGMSTEP--VINTYANFRDVIYPRKIL 345
Cc 131 DSGWQKKRKRKLTDP-----WITELHNGSKKKRPGFRFYRMADELIFVLER 183
Cc 346 GYNVOLAIOESHYYASGCVHTNIFYAASRFGTDDLSLIDKAHELGLVLMIDYHS 405
Cc 184 GFTHELEPLVHPLDRSGYQGTGYSTYSKYGPHCFMVFVDCHOAGLVIIDWPG 243
Cc 406 HASTNLOGLNFDGTDGHYFHSRGRHMMWDSRLFNYSGWELREFLLSNARWMLDEYK 465
Cc 244 HECKDA-HELTYMFGDAPYEEYANERKRENYWGTANFDIGKPEVNSFLISNALFWLEYH 302
Cc 466 PDGFRFDGVTSMMYTHNGLOVDFGTGNNEFYGYADVAVVYLMILNDMIGLFEPAVTI 525
Cc 303 YDGFYDAVANLWPNNDRL---YENPY-----AVEFLQNLNAVAYDPHWMI 350
Cc 526 GDVSGMPTVCIPVEDGCVGFDYRLHMAVADKWEIIOKRDEDMKGIYVMTL----- 579
Cc 351 ADSDTDMPRTVAPTYDGGIGFNYK-----NMGMMNDMLKYIETPP 391
Cc 580 -NRWLEKCVS-----YAE-----SHQDALVGDKTIAFWLMDKMDYDFALDRPSTPL 626
Cc 392 HERKTAHNGVSPSLIYASENPILEFHSDEYVHGKSL----- 429
Cc 627 IDRGVALHKM-----TRITMGIGEGY-----LNMGNFEFGH-PEW----- 662
Cc 430 -----LNKMGSTYEKRAQLKL-----YGYMAHNGKLLPWGSEFFQFDMTAE 477
Cc 663 -----IDPRGDLHPSGKFPVGNNSYDKCRRRDLGNSKHLRYHGMQFQDAIYHLE 717
Cc 478 LDWVLEDF---ELHKKMEYVKOLIACTKRYKPYELD-----HDPREGWIDVINA 527
Cc 718 AVGEMTSEHOYISR-KDERDRIYFERGNLVFVNFHTSSYDYRVGCLKPGKYI;YLD 776
Cc 528 -----QSIFSEFIRKCKBGD-----VLIVYCNF--TNOAYDYKVSVPPLAPYHEVLN 573
Cc 777 SDDPLGFGFGRLS 789
Cc 574 SDAAEFGSGSHVN 586

RESULT 13
GLGB_BUTFI STANDARD: PRT: 639 AA.
ID GLGB_BUTFI
AC P30539;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)

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ACT SITE 464 464 BY SIMILARITY  
FT ACT SITE 532 BY SIMILARITY  
SEQUENCE 731 AA; 81729 MW; EE2BEF76532617 CRC64;

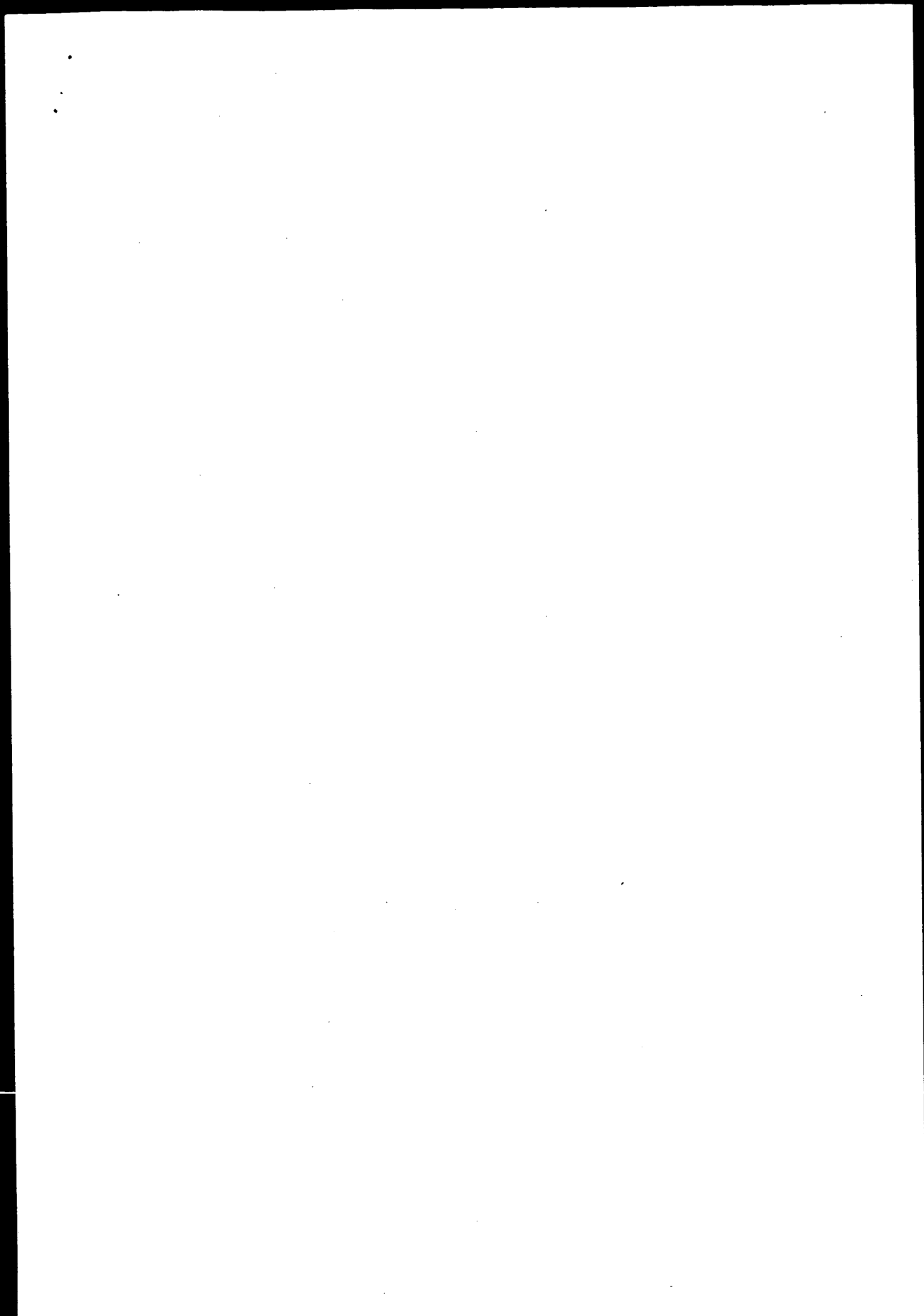
Query Match 11.58; Score 524.5; DB 1; Length 731;  
Best Local Similarity 24.78; Pred. No. 2.1e-30;  
Matches 187; Conservative 119; Mismatches 258; Indels 193; Gaps 32;

OC 131 GSKPRISPPRGORIVYDIDSLTGFROHLDYRSQYKRLREEDIKYEGSLDAFSRGEK 190  
DB 94 GCEPHTVAD-----AYRFLPTLGEVDLHL-FAAGRHREHLEWVGAPHR----- 136  
OC 191 GGFGRSE---TGITYREMAPGATMAALIGDFNNMNP-ADVMTONEGVWEIPL----- 241  
DB 137 -FTTADGVGVSPFAVAPNAKGVSLIGEFNGMNGHEAPRYLGPSCGWELFWPDPD 194  
OC 242 -NNAGD-----SEPIPHGSRYKIRMDTFSGNKDSIPAWIKFSVOAPGELPYNGI 289  
DB 195 GLYKRVVAGADGVYTDRAADPAFGEVP--PQTASRYTSSTYTWGDDMMAGRLL----- 247  
OC 290 YYDPPEEKYVFKNDQPKRPSLRVESHVGMSTSEPTINTYANFRDYLPRIKKLYNA 349  
DB 248 ------RNFV---NEAMSTYEHLG--SWRPEL-SYROLARLTDYIVDQGFTH 289  
OC 350 VOLMAIQEHSTYASFGYVNTFYAASSRFGTPDDKSLIDKAHELGLLVMDIVHSHAST 409  
DB 230 VELLVAHEPFRAGSWGIVYVAPTSTSRFGTPDFRALVDALHOAGIGVYDWPVAFPK 349  
OC 410 NTLDLGNFDTGDIHYEHSR- RGHMMWMSRLNYSWEVLEFLLSNARWMLDEYKFDG 468  
DB 350 DAM-ALGRFFDTP-LYEHSDPKRGEOLDMGTYVDFPGRPEVRNLFVANALYLOEFHIDG 407  
OC 469 FRFDGVTSMATYTHGL-QVDFTGNVNEFYGATVDNAVYLMMLNDMIHGLPEAVTIGE 527  
DB 408 LRVAVASMLTLDYSRPGGWTPNVH--GGRENLEAVQFLOENNAATAHKAPGIVTIAE 464  
OC 528 DVSGPRTYCIYEDGVGVDFYRLHMAVADKWEIIOKDEDMKMDIYHMLTNRMKEK 587  
DB 465 ESTPMSVTRTPTNIGLGFSMK-----MNNG-----WMHDT 495  
OC 588 VSYAE-----SHDQAVGDDTIAFYLMDKMYDFMA 618  
DB 496 LDYVSROVYVSYHHNHTFMSLYAFSENLYPLSHDEYVHGKTL--WGR----- 544  
OC 619 LDRSTPLIDRGVALHKMIRLITMGLOGEGYLTNMGNEFG-HPFW-----IDPRGDLHL 672  
DB 545 -MEGNHNV-KAAGLRSLAYQMAHPGKO--LTFMGQGFGRGAWMSQRGIDWFOLD-- 596  
OC 673 PSGRFVPGNNYSYDKCRRRFDLGNKHLRHGMOEQFOALQHLEAVGFMTS-----EH 726  
DB 597 ------ENGFS-----NGIQLVADIDIDYIRCHPALMSLDTTPEGY 631  
OC 727 QYISKRDERRIIVER-----GNLVEFVNFHMTSSYDYRVGCLKPGKYKVLSDPDL 781  
DB 632 SWIAMSANNVLYFSFMRGSDGLVACVFNFA-GAEHRDYLDLPRAGRMREVINTDATI 690  
OC 782 FGGFRLSHDAEHFSFEGWYNDNRPSFVYVYPCRTAV 818  
DB 691 YHSGIGNLGVADATDPMH-GRPASAVLVLPPTSAL 726  
RESULT 15  
GLGB\_BACSU STANDARD; PRT; 627 AA.  
AC P39118;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 13-DEC-1998 (Rel. 37, Last annotation update)  
DE 1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) (GLYCOSYL BRANCHING ENZYME).  
GN GLGB.  
OS Bacillus subtilis.

OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Bacillus.  
OC NCBI\_Taxid=1423;  
RN (1)  
RN SEQUENCE FROM N.A.  
RC STRAIN=168;  
RC MEDLINE=94195107; PubMed=8145641;  
RA Kiel J.A.K.W., Boels J.M., Belman G., Venema G.;  
RT "Glycogen in Bacillus subtilis: molecular characterization of an operon encoding enzymes involved in glycogen biosynthesis and degradation.";  
RL Mol. Microbiol. 11:203-218(1994).  
RN (2)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98048467; PubMed=9387221;  
RA Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.;  
RT "Sequencing and functional annotation of the Bacillus subtilis genes in the 200 kb rmb-dnaB region.";  
RL Microbiology 143:3431-3441(1997).  
CC -1- FUNCTION: CATALYZES THE FORMATION OF THE ALPHA-1,6-GLUCOSIDIC LINKAGES IN GLYCOSACCHARIDE FROM GROWING ALPHA-1,4-GLUCAN CHAINS AND THE SUBSEQUENT TRANSFER OF THE OLIGOSACCHARIDE TO OTHER PARTS OF ALPHA-1,4-GLUCAN CHAINS.  
CC -1- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF GLYCOSYL TRANSFERASE.  
CC -1- PATHWAY: THIRD STEP IN GLYCOSYL BIOSYNTHESIS.  
CC -1- INDUCTION: EXPRESSED EXCLUSIVELY ON MEDIA CONTAINING CARBON SOURCES THAT ALLOW EFFICIENT SPOULATION.  
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.  
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CC  
CC EMBL: Z25795; CAAB1040.1;  
CC EMBL: AF008220; BAC00214.1;  
CC EMBL: Z29119; CAB15076.1;  
CC PIR: S36624; S36624.  
CC Subtilisin; B610907; 9198.  
CC InterPro: IP000461;  
CC Pfam: PF00128; alpha-amyase; 1.  
CC Glycogen biosynthesis; transferase; glycosyltransferase.  
CC ACT\_SITE 309 309 BY SIMILARITY.  
CC ACT\_SITE 352 352 BY SIMILARITY.  
CC ACT\_SITE 420 420 BY SIMILARITY.  
SQ SEQUENCE 627 AA; 73665 MW; 64B0A553B6767BA CRC64;  
Query Match 11.4%; Score 518.5; DB 1; Length 627;  
Best Local Similarity 26.9%; Pred. No. 4.6e-30;  
Matches 175; Conservative 106; Mismatches 254; Indels 115; Gaps 24;  
OC 177 YESSLAFAFGKGYEKFGRSE---TGITYREMAPGATMAALIGDFNNMNPADVATQ-N 231  
DB 15 HEGSSL--FKSYQLGRSHRELNGKSGYEFYVMAHASEVRAVAGDFNMSGGEHYVHRVN 71  
OC 232 ECGWEIPLNNADSGSPRIPHGSRYKIRMDTPSGN-KDISPAMIKFSVOAP--GEIPLYNG 288  
DB 72 DNGIWTLPFG-----IGEKERYKLEYVINGELRLKADYALYSEVRPTASITDL 124  
OC 289 IYDPPEEKYVFKNDQPKRPSLRVESHVGMSTSEPTINTYANFRDYLPRIKKLG 346  
DB 125 EGSWODQWOKRQAKTLYEKPVLYELHLGSMKHSGRYSYKELSGTLPIPKKHG 184  
OC 347 YNAVOLMAIQEHSTYASFGYVNTFYAASSRFGTPDDKSLIDKAHELGLLVMDIVHSH 406  
DB 185 FTHIELLPYEHPRDSRWGVOCTGYSPTSRPGPHDLMKFVDECHOONIGVILDVVPGH 244

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OY 407 ASTNTLDGLMFDGTGHTFHSGPRGHMMDSRLFNYSWEVLRFLLSNARWMLDEYKF 466
Db 245 FCKDA-HGLYMFDEGLYEXKERDRRENMLMGTFANFDLGRPEVHSFLISNALYNAEFYHI 303
OY 467 DGRFDGVTSMYTHHGLQVDFTGNVNEYFGVATDVAVVYLMLLNDMIGHLPFEAVTIG 526
Db 304 DGRVDVANILX-----WPNODERH---TNFYAVDFLKRKNQJMRREAYPHVMIA 351
OY 527 EDVSGMPVCIPEYDGGVGFYRLHMAVADKWVEIIQKRDWDWKGDIIVHL---TNRR 582
Db 352 EDSTEMPQVYTGAVEEGGLGFHYKMMG-----W-MNDVLYKMETPPEERR 395
OY 583 WLEKCVSYA-----ESHDAVGDKTIAEWLMDK---DWTDFMALDRPSTPLI 627
Db 396 HCHQLISFSLYAFSEHFVLPFSHDEVYGGKS---LTKMPGDYWKFAQYR---LL 447
OY 628 DRGVALHKMIRLITMGLGGEGYLNFMGNERGH-PEMIDFPRGD-----LHLPBGKEVP 679
Db 448 LGYMTYHPGKLL-----FMGSEFAQFDEMDTEQLDWFLDSFPMHOKASVFTQ 496
OY 680 GNNYSYDKCRRRPDLGNSKHLRYHGMQEPDOAIQHLLEAYGFMTEHQYISRKDERDRII 739
Db 497 DLLRFYQKSKILIY-----HDHRAQSFEMIDVHNDEQSI--SFIRYQKNGEA---- 543
OY 740 VFERGNLVFENFHTSSYSQYRVCGLKPGKYIVLDSDDPLFGGGRLS 789
Db 544 -----LVYICNF-TPVYVHQYDVGVPFFTYQYLEVLSNDSSEYGGSGQIN 586
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Search completed: August 7, 2001, 11:20:44  
Job time: 141 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 7, 2001, 11:18:23 ; Search time 14.99 Seconds

(without alignments)  
1910.446 Million cell updates/sec

Title: US-09-297-703A-29

Perfect score: 4545

Sequence: 1 MGVYRTSGIRPCAPLCKSQ.....AVYALVDEVEENLEPVAG 836

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3160	69.5	799	1	GLGB_MAIZE
2	2145	47.2	861	1	GLGB_SOLNU
3	2130.5	46.9	820	1	GLGB_ORYSA
4	2049	45.1	702	1	GLGB_HUMAN
5	1765.5	38.8	704	1	GLGB_YEAST
6	604.5	13.3	773	1	GLGB_SYN7
7	587	12.9	770	1	GLGB_STN3
8	572	12.6	639	1	GLGB_BACST
9	571.5	12.6	728	1	GLGB_ECOLI
10	566	12.5	730	1	GLGB_HAEIN
11	542.5	11.9	734	1	GLGB_AGRU
12	539.5	11.9	666	1	GLGB_BACCI
13	533.5	11.7	639	1	GLGB_BUTRI
14	524.5	11.5	731	1	GLGB_MYCTU
15	518.5	11.4	627	1	GLGB_BACSV
16	478.5	10.5	764	1	GLGB_STRAV
17	227.5	5.0	580	1	YF62_MYCTU
18	211.5	4.7	721	1	GLGX_MYCTU
19	207	4.6	843	1	PURA_THENA
20	189.5	4.2	657	1	GLGX_ECOLI
21	187	4.1	1196	1	AMYB_PAEPO
22	180.5	4.0	494	1	AMY1_SACPI
23	180	4.0	562	1	AMY2_DICHT
24	179	3.9	574	1	CDAS_THERT
25	172.5	3.8	498	1	AMY3_DICHT
26	172	3.8	508	1	MAU1_DROME
27	168	3.7	588	1	NEPU_BACST
28	167	3.7	584	1	MA1S_YEAST
29	167	3.7	584	1	MA3S_YEAST
30	166	3.7	584	1	MA6S_YEAST
31	165	3.6	659	1	GLGX_HAEIN
32	164	3.6	522	1	MA12_DROME
33	161	3.5	549	1	AGLA_RHIME

34	158.5	3.5	777	1	ISOA_FLASP
35	158	3.5	508	1	MA13_DROME
36	157.5	3.5	505	1	016G_BACSP
37	156.5	3.4	591	1	CDAS_BACSH
38	155.5	3.4	484	1	AMYA_ASPNG
39	152	3.3	581	1	MAXS_YEAST
40	151	3.3	555	1	016G_BACCO
41	150.5	3.3	676	1	AMYL_ECOLI
42	150	3.3	478	1	YDD1_SCHPO
43	149.5	3.3	557	1	AGL_PEPDE
44	149	3.3	776	1	ISOA_PSEAY
45	149	3.3	776	1	ISOA_PSESP

## ALIGNMENTS

RESULT ID	GLGB_MAIZE	STANDARD	PRT	799 AA.
AC	008047;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	1,4-ALPHA-GLUCAN BRANCHING ENZYME IIB PRECURSOR (EC 2.4.1.18) (STARCH BRANCHING ENZYME IIB) (O-ENZYME).			
GN	SBE1.			
OS	Zea mays (Maize).			
OC	Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;			
OC	Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae;			
OC	Andropogoneae; Zea.			
OX	NCBI_TaxID=4577;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 58-65.			
RC	STRAIN=CY. W64A X 182E; TISSUE=Endosperm;			
RA	MEDLINE=94105320; PubMed=8278524;			
RA	Fisher D.K., Boyer C.D., Hannah L.C.;			
RT	*Starch branching enzyme II from maize endosperm.*;			
RL	Plant Physiol. 102:1045-1046(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 248-271 AND 305-315.			
RC	STRAIN=CY. B73; TISSUE=Endosperm;			
RX	MEDLINE=95152344; PubMed=7849565;			
RA	Guan H.P., Baba T., Preiss J.;			
RT	*Expression of branching enzyme II of maize endosperm in Escherichia coli.*;			
RL	Cell. Mol. Biol. 40:981-988(1994).			
CC	-1- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF GLYCOGEN.			
CC	-1- PATHWAY: THIRD STEP IN STARCH BIOSYNTHESIS.			
CC	-1- SUBUNIT: MONOMER (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: AMYLOPLAST.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.			
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CC	-----			
DR	EMBL; L08065; AAA18571.1; -.			
DR	MAizedB; 63943; -.			
DR	Mendel; 16392; ZEma; sm16392.			
DR	InterPro; IPR000461; -.			
DR	Pfam; PF00128; alpha-amylase; 1.			
KW	Glycogen biosynthesis; transferase; glycosyltransferase; Chloroplast;			
KW	Transit peptide; Amyloplast; starch biosynthesis.			
FT	TRANSIT 1 57			
FT	CHAIN 58 799			
FT	ACT_SITE 394 394			
FT	BY SIMILARITY.			

FT ACT\_SITE 447 447 BY SIMILARITY.  
 FT ACT\_SITE 516 516 BY SIMILARITY.  
 SO SEQUENCE 799 AA; 90517 MW; 0B440E0377B8087A CRC64;

Query Match 69.5%: Score 3160; DB 1; Length 799;  
 Best Local Similarity 70.3%; Pred. No. 5.2e-222;  
 Matches 583; Conservative 83; Mismatches 95; Indels 68; Gaps 8;

QY 2 GHYTSIGTRPCAPLCKSQSGTGFGRRTSSCLSPNEAFSRVFGSKSHEDSSVM 61  
 DB 33 GLETRGARVGC-----SOTHAMRAA-----MAARKA-----YM 62  
 QY 62 VYAKRVLPGD---RIEYSSSTDLLEAPGVSESYQ---LTVESIIMDKIVEDEVN 115  
 DB 63 YPEGN---DGLASRADSAQFOSDELEVP-DISEETGAGVADAQAL----- 106  
 QY 116 KESVPMRETVSIRKIGSKPRSTIPPPRGQRIYDIPSLTGRQHLDIRYQYKRLREID 175  
 DB 107 -----NRKRVVPPSDQKIFQIDPMQGIKYLEYKSLKRLKSID 150  
 QY 176 KYEGSIDAFSRGCEKFGESRSETGITYREMAPGATWALLIGDENMNPADVMTONEGCV 235  
 DB 151 EHBGGLEAFSRSEYERGFVAFSAEGITYREMAPGAFSAALGVGNMNPADKRSNERGV 210  
 QY 236 WEIFLNNADGSPPIPHGSRVAKIRMDTPSGNKSIPAMIKESVQAPGELPYNGITYDPE 295  
 DB 211 WEIFLNNADGSPPIPHGSRVAKIRMDTPSGNKSIPAMIKESVQAPGELPYNGITYDPE 270  
 QY 296 EEEYVFRHAPKPKKSLRIYETHVGSSEPEKINITYVNRDEVLPRIKKLGYNVQALMAI 355  
 DB 271 EYVYVFRHAPKPKKSLRIYETHVGSSEPEKINITYVNRDEVLPRIKKLGYNVQALMAI 330  
 QY 356 QEHSYAFSGYHNTNYAASSRFGTPDDKSLDKAHELGILVMDIVHSHASTNLLDGL 415  
 DB 331 QEHSYAFSGYHNTNYAASSRFGTPDDKSLDKAHELGILVMDIVHSHASTNLLDGL 390  
 QY 416 NMEDGTDGHHFSGRGMHMMDSRLFNYSMEVLFRLSLNARWMLDEKFGFREDGYT 475  
 DB 391 NGEDGTDGHHFSGRGMHMMDSRLFNYSMEVLFRLSLNARWMLDEKFGFREDGYT 450  
 QY 476 SMATYTHGLQVDTGNYNEFGATGVDVAVYMLINDMIHGLFPRAVIGEDVSGMPTV 535  
 DB 451 SMATYTHGLQVDTGNYNEFGATGVDVAVYMLINDMIHGLFPRAVIGEDVSGMPTV 510  
 QY 536 CTFEDGSGVGFEDYRLHMAVADKVEITQKDEDEWKKGDIVHMLTNRWTEKCYAESH 595  
 DB 511 ALPHVDGSGVGFEDYRLHMAVADKVEITQKDEDEWKKGDIVHMLTNRWTEKCYAESH 570  
 QY 596 QALVGDKTIAFWLMDKMDYFMAALDRPSTPLIDRGVALHMKIRLITMGJGEGYLNFGN 655  
 DB 571 QALVGDKTIAFWLMDKMDYFMAALDRPSTPLIDRGVALHMKIRLITMGJGEGYLNFGN 630  
 QY 656 EFGHEPIDPPRGDLHLPSCGFYVGNNTSYDKCRREDLGNKHLRYHGOEFDQAIOHL 715  
 DB 631 EFGHEPIDPPRGDLHLPSCGFYVGNNTSYDKCRREDLGNKHLRYHGOEFDQAIOHL 690  
 QY 716 EEAAGFMTSEHOYTSRKOEDRIIVFERGNLIVFNFHMTSSYSDYKRVGCLKPGKYIYL 775  
 DB 691 EEAAGFMTSEHOYTSRKOEDRIIVFERGNLIVFNFHMTSSYSDYKRVGCLKPGKYIYL 750  
 QY 776 DSDPLTGGGFRGLSHDAEHFSEGMWYNNRPSFVNYPPCTAAVYALVE 824  
 DB 751 DSDPLTGGGFRGLSHDAEHFSEGMWYNNRPSFVNYPPCTAAVYALVE 799

DE 1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) (STARCH BRANCHING  
 ENZYME) (O ENZYME).  
 GN SBE1 OR SBE.  
 OS Solanum tuberosum (Potato).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; eusterids I;  
 OC Solanales; Solanaceae; Solanum.  
 OX NCBI:Taxid=4113;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. DIANELLA;  
 RX MEDLINE=94105324; PubMed=8278528;  
 RA Poulson P., Kreiberg J.D.;  
 RA "starch branching enzyme cDNA from Solanum tuberosum.";  
 RL Plant Physiol. 102:1053-1054(1993).  
 RN [2]  
 RP SEQUENCE OF 279-527 FROM N.A.  
 RC STRAIN=CV. DESIREE; Tissue=Tuber;  
 RX MEDLINE=92079917; PubMed=1745241;  
 RA Kosmann J., Visser R.G.F., Mueller-Roeber B., Willmitzer L.,  
 RA Sonnwald U.;  
 RT "Cloning and expression analysis of a potato cDNA that encodes  
 RT branching enzyme: evidence for co-expression of starch biosynthetic  
 RT genes.";  
 RL Mol. Gen. Genet. 230:39-44(1991).  
 CC -1- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF  
 CC STARCH.  
 CC -1- PATHWAY: THIRD STEP IN STARCH BIOSYNTHESIS.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SUBCELLULAR LOCATION: AMYLOPLAST.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO  
 CC KNOWN AS THE ALPHA-AMYLASE FAMILY.  
 CC  
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 CC  
 CC EMBL: X69805; CAA9463.1; -  
 CC PIR: S18594; S18594.  
 CC DR Mendel: 13376; Soltu; Sbel.1.  
 CC DR InterPro: IPR000461; -  
 CC DR Pfam: PF00128; alpha-amylase; 1.  
 CC KW Starch biosynthesis; transferase; glycosyltransferase; Amyloplast.  
 CC FT ACT\_SITE 424 424 BY SIMILARITY.  
 CC FT ACT\_SITE 484 484 BY SIMILARITY.  
 CC FT ACT\_SITE 553 553 BY SIMILARITY.  
 SO SEQUENCE 861 AA; 99083 MW; FAD519AC7CF1BE2 CRC64;

Query Match 47.2%: Score 2145; DB 1; Length 61;  
 Best Local Similarity 51.6%; Pred. No. 3.8e-148;  
 Matches 411; Conservative 116; Mismatches 183; Indels 86; Gaps 12;

QY 34 LSFNRK-----EAFSRVFGSKSH-----ESDSGIVAVYASKR 67  
 DB 1 MEINENVLSKPIRSGSPSPFSPVSSGASRNKICFSGHSTGLKSGQSRSMWISTPSKR 60  
 QY 68 VLPDGRICEYSSSTDLLEAPGVSESOYLDVDELINDDKIVEDEVKESVPMRETVSI 127  
 DB 61 VRDERMRK-HSSAI-----SAVLID-----DSTYMLPLEEDVKT 93  
 QY 128 RKIGSKRSPISPPRGQRIYDIPSLTGRQHLDIRYQYKRLREIDKYKESIDAFSRG 187  
 DB 94 ENIG-----LNLDPLEPLDIFRFRMRKRYDQKMLREYELPLEEFAOG 139  
 QY 188 YKFGSRSEGTGITYREMAPGATWALLIGDENMNPADVMTONEGCVWEITLNNADGS 247  
 DB 140 YLKFGRNREDGCIYREMAPGATWALLIGDENMNPADVMTONEGCVWEITLNNADGS 198

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QY 248 PRPHSGSRVAKIRMDTPSGN-KDISIPAMIKFSVOAPGEL--PINGIYYDDPEEKYVKNP 304
DB 199 PVPIDHMSRVRKFRKHHGNGVWVDRIIPAMIKYATADATKFAAPYDGVYDDPPPSERYHFXY 258
QY 305 QPRRPSLRIRYESHVSGMSTPEPIYNTYANPRDVLPRIKKLGNAVQALQESHYSAF 364
DB 259 RPKPRAPRIYEAHVAMSSSEPPVNSYREFADVLRIRAKANNNTVQALMAIMESHVYGSF 318
QY 365 GYHVTNFFYAASSRFGTTPDDLSLIDKAHELGILVLMIDYHSHASTWLDGLNMF--GT 421
DB 319 GYHVTNFFYAVSSRYGNPEDLKYLIDKAHSLGLVLDVYHSHASNVTYGLNFDGLQSS 378
QY 422 DGHYFHSGRGHMMWDSRLFNYSWEVLRFLLSNARWMLDEXKFDGFRFDGYTSMYTH 481
DB 379 QESYFHAAGEGRYHKLWDSRLFNANWEVLRFLLSNARWMLDEXKFDGFRFDGYTSMYTH 438
QY 482 HGLQVDFGTGNYNRYFGYADVDAVYVYLMMLNDMIRHLPFEPAYTIGDVGMPVYCV 541
DB 439 HGLNMGFTGNYNRYFEADVDAVYVYLMMLNLIHKIFPDATYIADVSGMPGLGRVSE 498
QY 542 GGYGFDFYRLMAVADKWEIIO-KRDEDMKGDIVHMLNRRMLEKCVSYAESHDQALVG 600
DB 499 GGIGFDFYRLMALIPDKVIDLKKNDKEDMSMKVTSLLNRRTTECIAYASHDSIYV 558
QY 601 DKTIAFWLMDKMDYFMAIDLRPSTPLIDRGVALHKKMIRLITMGLGEGYLNFMNGNEFHP 660
DB 559 DKTIAFWLMDKEMYSGLTSDASPYVDGRIALHKKMIRLITMGLGEGYLNFMNGNEFHP 618
QY 661 EMTDFPRGDLHLPSGKFVGNNGNSYDCKRRRPLDGSKILRHGMEFPOALQHELEANG 720
DB 619 EMTDFPRGDLHLPSGKFVGNNGNSYDCKRRRPLDGSKILRHGMEFPOALQHELEANG 667
QY 721 FMTSEHQYISRKDERDRIYFERNGLVFNFMHTSSYSDYRGCLPKPKYKIVLDSDDP 780
DB 668 FLASGQIYVSSMDDKVYVEFERGLDYFVFNHPRKTYGKYVGCGLPKKYVALDSDAM 727
QY 781 LFGGFRGLSHDAEHFS 796
DB 728 EFGGHRGTGHDVHFT 743

RESULT 3
GLOB_ORYSA STANDARD: PRT: 820 AA.
AC 001401;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE 1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) (STARCH BRANCHING
DE ENZYME) (Q-ENZYME).
GN SBEI.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae;
OC Oryza.
OC NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, JAPONICA; TISSUE=Endosperm;
RA Nakamura Y., Yamanouchi H.;
RT "Nucleotide sequence of a cDNA encoding starch-branching enzyme, or
RT Q-enzyme I, from rice endosperm."
RL Plant Physiol. 99:1265-1266(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93204882; PubMed=8455548;
RA Kawasaki T., Mizuno K., Baba T., Shimada H.;
RT "Molecular analysis of the gene encoding a rice starch branching
RT enzyme."
RL Mol. Gen. Genet. 237:10-16(1993).
CC -1- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF
CC GLYCOGEN.
CC -1- PATHWAY: THIRD STEP IN STARCH BIOSYNTHESIS.

```

```

CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: AMYLOPLAST.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC -----
DR EMBL: D10752; BAA01584.1; -
DR EMBL: D10838; BAA01616.1; -
DR InterPro: IPR000461; -
DR Pfam: PF00128; alpha-amylase; 1.
KW Starch biosynthesis; Transferase; Glycosyltransferase; Amyloplast.
FT MOD_RES 1
FT ACT_SITE 409 409 BY SIMILARITY.
FT ACT_SITE 464 464 BY SIMILARITY.
FT ACT_SITE 533 533 BY SIMILARITY.
FT CONFLICT 13 13 P -> A (IN REF. 2).
FT CONFLICT 715 753 VGHVDHFTSPDEGMVPEFNFNPNRPSFVLSPPETCV
FT -> LAMMWTISRLPRCEQEVOKOISTALTHSKSPRPV
FT PVM (IN REF. 2).
SQ SEQUENCE 820 AA; 93262 MM; A687CF9396F359DF CRC64;

Query Match 46.9%; Score 2130.5; DB 1; Length 820;
Best Local Similarity 54.5%; Pred. No. 4e-147;
Matches 401; Conservative 113; Mismatches 171; Indels 51; Gaps 11;

QY 132 SKPR-----SIPPGSGOR-----IYIDPSLNGFROHLYRSOY 167
DB 40 SSPRSNGKAYKTNFVSVALRKNTMYTVYEVVDHLPIYDLRLEBKDFHETRYKRY 99
QY 168 KRLREIDKRYGSLDPAFSRGYKFEFSRSETGITYREWAPGATAAALIGFNNMNPADV 227
DB 100 LDQKCLIEKHSGLEEFSGYGLKRGINTVDGATYREMAPAAQEOALIGFNNMNGAKKH 159
QY 228 MTQNECGVWEIFLPNNADSPPIPHGSRVYKIRMDTPSGN-KDISIPAMIKFSVOAPGEL-- 284
DB 160 MEKDKFGTMSIKI-SHVNGKPAIPHNSKVFRFRGGGAWADRIIPAMIRYATFPASFGA 218
QY 285 PYNGIYVPRPEBEKVFKNPOPKRPSLRIRYESHVSGMSTPEPIYNTYANPRDVLPRIKK 344
DB 219 PYDGHMPPACERIVFHPRPKPDAPRIYEAHVAMSSSEPPVSYREFADVLRIRAK 278
QY 345 LGYNAVQALMAIOESHYSAFSGYHVTNFFYAASSRFGTTPDDLSLIDKAHELGILVLMIDYH 404
DB 279 NNYNNTVQALMAIMESHYSAFSGYHVTNFFYAASSRSGTPEDLKYLIDKAHSLGLRLMDYVH 338
QY 405 SHASTNTLDGLNMF--GTGSH--YFHSGRGHMMWDSRLFNYSWEVLRFLLSNARWML 461
DB 339 SHASNNTVDGLNGYVGCGNTSESYFHTGDRGYHKLWDSRLFNANWEVLRFLLSNLRHYM 398
QY 462 DEYKDFGRFPDGVNSMWTYHGLQVDFGTGNYNRYFGYADVDAVYVYLMMLNDMIRHLPF 521
DB 399 DEYKDFGRFPDGVNSMWTYHGLQVDFGTGNYNRYFGYADVDAVYVYLMMLNDMIRHLPF 458
QY 522 AVTTGEDVSGMPYVCIPEDEGVGFDYRLHMAVADKWEIIO-KRDEDMKGDIVHMLTN 580
DB 459 ATIVAEVSGMPVLCRPDEBGVGFDFLMAAIPDRWTDYLNKNEEDKMSMSEIVQTLTN 518
QY 561 RRMLEKCVSYAESHDQALVGKTTAFWLMKMDYFMAIDLRPSTPLIDRGVALHKKMIRLI 640
DB 519 RRYTEKCIAYASHDSIYVGDKTITAFLLMDKEMYTGSNDLPASPTINRGIALQKMHFI 578
QY 641 TMGLGEGYLNPMGNEFHPMDIPPRGDLHLPSGKFVPGNNSYDCKRRRPLDGSKILH 700
DB 579 TMALGGDGLTNFMNGNEFHPMDIPR-----EGNNSYDCKRRRPLDGSKILH 627

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Qy	701	RYHGMDFEFOALHLEENYAGFMTEHGYISRKDEBRIVLFEKGNIVLEVFNNHMTSSYD	760
Db	628	RYKYMAAFQOANNALEEFESFLSSSKQIVADMNEKRVLFERGDIVLFVNHPHKKTYKG	687
Qy	761	YRKGCGLPKPKRYIVLSDDPLEFGFGRLSHDAHF-SPEGM-----YDNPRESFMVYT	812
Db	688	YKYGCDLPKRYHVALDSQALFEGHGVRGHDVHFTSPSGMGVPEPTNNRNPNSFKYLS	747
Qy	813	PCRTAYVALVEEYE	828
Db	748	PPRTCAIYRYVDEKRE	763

RESULT	4	
GLGB_HUMAN		
ID	GLGB_HUMAN	STANDARD;
AC	0044A6.	PRT; 702 AA.

DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE 1.4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18)  
 GN ENZYME) (BRANCHER ENZYME).  
 GN GAB1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID:9606;

RP SEQUENCE FROM N.A.  
RC TISSUE-LIVER: PubMed=93216700; Thon V.J., Khaili M., Cannon J.F.  
RA MEDLINE=93216700; Thon V.J., Khaili M., Cannon J.F.  
RT "Isolation of human glycogen branching enzyme cDNAs by screening  
TT complementation in yeast."; J Biol Chem. 268:7509-7513(1993).  
RI J Biol Chem. 268:7509-7513(1993).  
CC -1- FUNCTION: REQUIRED FOR SUPERFICIENT GLYCOGEN ACCUMULATION. THE  
CC ALPHA-1,6 BRANCHES OF GLYCOGEN PLAY AN IMPORTANT ROLE IN  
CC INCREASING THE SOLUBILITY OF THE MOLECULE AND, CONSEQUENTLY, IN  
CC REDUCING THE OSMOTIC PRESSURE WITHIN CELLS.  
CC -1- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF  
CC GLYCOGEN. PMID=75097513

CC -1 SUBSTRATE MONOMER. CC  
CC -1 TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN LIVER AND MUSCLE. CC  
CC DISEASE: DEFECTS IN G6PI ARE THE CAUSE OF GLYCOGEN STORAGE DISEASE CC  
CC IV (GSD-IV) (ALSO KNOWN AS ANDERSEN'S DISEASE); A RARE FORM OF CC  
CC GLYCOGENOSIS CHARACTERIZED BY THE ACCUMULATION OF ABNORMALLY CC  
CC STRUCTURED GLYCOGEN THAT RESULTS IN EARLY ONSET HEPATIC CIRRHOSIS, CC  
CC CARDIAC ARREST AND NEUROMUSCULAR DISEASES. MOST CHILDREN WITH THIS CC  
CC CONDITION DIE BEFORE TWO YEARS OF AGE. NO TREATMENT APART FROM THE CC  
CC LIVER TRANSPLANTATION HAS BEEN FOUND TO PREVENT PROGRESSION OF THE CC  
CC DISEASE. CC  
CC -1 SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO CC  
CC KNOWN AS THE ALPHA-AMYLASE FAMILY. CC  
CC  
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DR	EMBL; L07956; AAA58642.1;	-.
DR	MIM; 232500;	-.
DR	Interpro; IPR0018;	alpha-amylase; 1.
DR	Pfam; PF00128;	Glycogen biosynthesis; Transfease; Glycosyltransferasee
KW	Glycogen storage disease.	
FT	ACT_SITE	357 357
FT	ACT_SITE	412 412
FT	ACT_SITE	481 481
FT	SQ	702 AA; 804/3 NM; 4B33AABD35BAFEF3 CRC64;
FT	SOURCE	

[illegible]

RESULT	5			
GLGB_YEAST				
ID	GLGB_YEAST	STANDARD:	PRT:	704 AA.
AC	P32775;			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	01-FEB-1995 (Rel. 31, Last annotation update)			
DE	1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) (GLYCOGEN BRANCHING ENZYME).			
GN	GLC3 OR YEL011W.			
OS	Saccharomyces cerevisiae (Baker's yeast).			
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;			
OC	Saccharomycetales; Saccharomycetaceae; Saccharomycus.			
OX	NCBI_TaxID=4932;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=92340578; PubMed=1634552;			
RA	Thon V.J., Vigneron-Lesens C., Marianne-Pepin T., Montreuil J.,			

RA Deeg A., Rachez C., Ball S.G., Cannon J.F.;  
 RT "Coordinate regulation of glycogen metabolism in the yeast  
 RT *Saccharomyces cerevisiae*. Induction of glycogen branching enzyme.";  
 RL *J. Biol. Chem.* 267:15224-15228(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN: S288C / AB972;  
 RA Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,  
 RA Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.,  
 RA Chung E., Duncan M., Guzman E., Hartzell G., Hunkle-Smith S.,  
 RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,  
 RA Meschede D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,  
 RA Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,  
 RA Taylor P., Wei Y., Yellon M., Botstein D., Davis R.W.;  
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF  
 CC GLYCOGEN.  
 CC -1- PATHWAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING THE TRANSITION BETWEEN THE  
 CC LATE EXPONENTIAL AND STATIONARY GROWTH PHASES, COINCIDENT WITH  
 CC MAXIMAL GLYCOGEN ACCUMULATION.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO  
 CC KNOWN AS THE ALPHA-AMYLASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: M76739; AAA34632.1; -  
 DR EMBL: U18530; AAB64488.1; -  
 DR PIR: A42752; A42752.  
 DR SGD: S0000737; GLC3.  
 DR InterPro: IPR000461; -  
 DR Pfam: PF00128; alpha-amylase; 1.  
 DR GlycoGen biosynthesis; Transferrase; Glycosyltransferase.  
 FT ACT SITE 356 356 BY SIMILARITY.  
 FT ACT SITE 417 417 BY SIMILARITY.  
 FT ACT SITE 486 486 BY SIMILARITY.  
 FT ACT SITE 564 564 S -> T (IN REF. 1).  
 FT CONFLICT 564 564  
 SQ SOURCE 704 AA; 81115 MW; 9C2227E107B825F27 CRC64;

Query Match 38.8%; Score 1765.5; DB 1; Length 704;  
 Best Local Similarity 50.6%; Pred. No. 1,le-120;  
 Matches 367; Conservative 109; Mismatches 190; Indels 59; Gaps 19;

QY 136 SIPPGRGQRIYDIDSLGFRQHLDRYSQYKRLREIDKY-----EGSIDAFSR 186  
 DB 3 NIDDNKKG-AVEFDPLWLPFADVLSE-----RYLADKWLVTITATPDGSGQSLSK 53  
 QY 187 -----GYEKGF-SRSEET-GITREMAPGATMAALIGDFNNMNPNA-DVATONECCEWEIF 239  
 DB 54 FARDYSKYGLAHNPETKEITKYEMAPNARAFIVGDFNMOTSHELKNDDEGENFTIT 113  
 QY 240 LPMNAGSGPPIPHGSRVKTIRMDTPSGNK-DSTIPANIKTSVQAPGEL-----PYNGIYD 292  
 DB 114 LHPDPGDAFLPDSKIKWFTLPDGSIFRLPAMITRATOPSKETSKQFGAPEGKRW 173  
 QY 293 PPEEYVFNKPNQPRPK---SLRIYESHVGMSTPEVINYANRDVLPRIKLGNA 349  
 DB 174 P--ENYKRVHPRKSEVSDSLRIYEAHVIGSSPEKITTYKTEFTEVLPRIKLGDA 231  
 QY 350 VOLMAIOEHSYASFGYHTVNFYAASRFGTDDLSKLIDKAHEGLGLVLDIVHSHAST 409  
 DB 232 IQMAIMEAHAYVASRGYQTNFFAASRRCPEELKEILDRAHSGILVLDVYHSHASK 291  
 QY 410 NTLDGANMFDGIDGATFH--SGPRGHMMWDSRLFNYSWEVLRLSNAMWMLDEKFD 467  
 DB 292 NVEDGLNMFDSHDQYFHSISSGRGEHPLMDSRLFNYSKFEVQRLANLAFFYDVYQFD 351

QY 468 GRPDGVTSMATTHHGLGV--DEFGNTNEYFG---YATDVDAVYVLTMLNDMTHGLPEP- 521  
 DB 352 GRRPDGVTSMATTHHGLGV--DEFGNTNEYFG---YATDVDAVYVLTMLNDMTHGLPEP- 521  
 QY 522 AVTIGEDVSGMPYICIPEDGSGVGFDRILMAVADKVEII-QKREDKMGDIYMLTN 580  
 DB 412 AVTAEDVSGMPYICIPEDGSGVGFDRILMAVADKVEII-QKREDKMGDIYMLTN 580  
 QY 581 RRMLEKVSVAESHDQALVGDITAFWLMMDKMT-DEPMALDRSPKLDIRGVALHMTL 639  
 DB 472 RRYGKVAVAVESHDQALVGDITAFWLMMDKMT-DEPMALDRSPKLDIRGVALHMTL 639  
 QY 640 ITMGLGEGYITNFMNGNEHPEWIDPEPGLHPPSGKEVYGNYSYDKORRREDLGNK 699  
 DB 531 ITMGLGEGYITNFMNGNEHPEWIDPEPGLHPPSGKEVYGNYSYDKORRREDLGNK 699  
 QY 700 LRYHMOEFODALIHLAENGAFMTSEHQYISKRDERDRIYFERGLVYVFNHMTSIS 759  
 DB 580 LRYONLEFDSMOLCKRRHMTKQAVYSLKHEDDKMIVFERNNMLFIYFNHMTSIS 759  
 QY 760 DYRGCIKPKYKIVLDDSDPLFGFGFRLSHDAEHSFEGWYDNRPRSPMYTTPCETAV 819  
 DB 640 DYRGVAKAGYHIVLNSDRAEFGGHNRIKINSEFFTTDLEMNNKNTLVYIPSRVALY 699  
 QY 820 YALVE 824  
 DB 700 LALKE 704

RESULT 5  
 ID GLGB\_SYNP7 STANDARD; PRT; 773 AA.  
 AC P16954;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 01-FEB-1995 (Rel. 31, Last annotation update)  
 DE 1.4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) (GLYCOGEN BRANCHING  
 DE ENZYME).  
 GN GLGB.  
 OS *Synechococcus* sp. (strain PCC 7942) (*Anacystis nidulans* R2).  
 OC Bacteria; Cyanobacteria; Chroococcales; *Synechococcus*.  
 OX NCBI\_TaxID=1140;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90323609; PubMed=2142668;  
 RA Kiel J.A.K.W., Boels J.M., Belman G., Venema G.;  
 RT "Nucleotide sequence of the *Synechococcus* sp. PCC7942 branching  
 RT enzyme gene (glgB): expression in *Bacillus subtilis*.";  
 RL *Gene* 89:77-84(1990).  
 CC -1- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF  
 CC GLYCOGEN.  
 CC -1- PATHWAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- MISCELLANEOUS: THE TEMPERATURE FOR OPTIMAL ACTIVITY IS  
 CC APPROXIMATELY 35 DEGREES CELSIUS.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO  
 CC KNOWN AS THE ALPHA-AMYLASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: M31544; AAB39038.1; -  
 DR PIR: J00550; J00550.  
 DR InterPro: IPR000461; -  
 DR Pfam: PF00128; alpha-amylase; 1.  
 KW GlycoGen biosynthesis; Transferrase; Glycosyltransferase.  
 FT INIT\_MET 0 0



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OM protein - protein search, using sw model

Run on: August 7, 2001, 11:17:58 ; Search time 31.12 Seconds

(without alignments)  
3554.210 Million cell updates/sec

Title: us-09-297-703a-29

Sequence: 1 MGRITGIRPPCAPLCKSQ.....AVYALVEDEVELEFPVAG 836

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 133305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: SP-archaea:.\*  
2: SP-bacteria:.\*  
3: SP-fungi:.\*  
4: SP-human:.\*  
5: SP-invertebrate:.\*  
6: SP-mammal:.\*  
7: SP-mhc:.\*  
8: SP-organelle:.\*  
9: SP-phage:.\*  
10: SP-plant:.\*  
11: SP-rodent:.\*  
12: SP-unclassified:.\*  
13: SP-vertebrate:.\*  
14: SP-virus:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3482.5	76.6	870	10 Q9XIS5	Q9XIS5 phaseolus v
2	3467	76.3	922	10 Q41058	Q41058 pisum sativ
3	3384.5	74.5	800	10 Q42531	Q42531 arabidopsis
4	3384.5	74.5	805	10 Q9LZS3	Q9LZS3 arabidopsis
5	3381.5	74.4	878	10 Q9XGA6	Q9XGA6 solanum tub
6	3373	74.2	858	10 Q23647	Q23647 arabidopsis
7	3360	73.9	871	10 Q9XGA5	Q9XGA5 solanum tub
8	3356	73.8	882	10 Q9XGA8	Q9XGA8 solanum tub
9	3343	73.5	830	10 Q49953	Q49953 solanum tub
10	3340	73.2	854	10 Q9XGA7	Q9XGA7 solanum tub
11	3327	72.9	854	10 Q42526	Q42526 arabidopsis
12	3315	71.8	814	10 Q9SXR9	Q9SXR9 oryza sativ
13	3261.5	71.7	823	10 Q24421	Q24421 zea mays (m
14	3260.5	71.6	823	10 Q9FU07	Q9FU07 triticum ae
15	3254.5	71.0	834	10 P93691	P93691 triticum ae
16	3225	70.6	729	10 Q9ZPB7	Q9ZPB7 hordeum vul
17	3209	70.0	825	10 Q24397	Q24397 triticum ae
18	3180	69.7	799	10 Q40663	Q40663 oryza sativ
19	3169	69.7	799	10 Q81387	Q81387 zea mays (m

20	3152.5	69.4	829	10 Q9ZTB6	Q9ZTB6 hordeum vul
21	2180	48.0	830	10 Q04864	Q04864 solanum tub
22	2165	47.6	810	10 Q9XGB3	Q9XGB3 triticum ae
23	2163	47.6	830	10 Q04074	Q04074 triticum ae
24	2163	47.6	833	10 Q9XGB1	Q9XGB1 triticum ae
25	2163	47.6	833	10 Q9ZUB8	Q9ZUB8 triticum ae
26	2163	47.6	865	10 Q9XGB2	Q9XGB2 triticum ae
27	2159	47.5	852	10 Q08131	Q08131 manihot esc
28	2143	47.2	832	10 Q9M6P8	Q9M6P8 sorghum bic
29	2134.5	47.0	847	10 Q9XIS4	Q9XIS4 phaseolus v
30	2130.5	46.9	820	10 Q40664	Q40664 oryza sativ
31	2124	46.7	823	10 Q41740	Q41740 zea mays (m
32	2107	46.4	807	10 Q9XED2	Q9XED2 triticum ae
33	2091.5	46.0	829	10 Q9XED3	Q9XED3 aegilops ta
34	2072.5	45.6	826	10 Q41059	Q41059 pisum sativ
35	1999	44.0	686	3 Q9Y8H3	Q9Y8H3 emeritella
36	1987	43.7	766	10 Q49185	Q49185 gracilaria
37	1976.5	43.5	733	3 Q9P5P3	Q9P5P3 neurospora
38	1897.5	41.7	865	5 Q9V6K7	Q9V6K7 drosophila
39	1885	41.5	681	5 Q22137	Q22137 caenorhabdi
40	1487	32.7	686	10 Q24393	Q24393 triticum ae
41	1351.5	29.7	433	10 Q9XGA9	Q9XGA9 solanum tub
42	1298	28.6	903	10 Q9LPP8	Q9LPP8 arabidopsis
43	778	17.1	190	10 Q9TON3	Q9TON3 solanum tub
44	769	16.9	189	10 Q9TON2	Q9TON2 solanum tub
45	669.5	14.7	187	10 Q9SSX6	Q9SSX6 nicotiana t

## ALIGNMENTS

RESULT	1	ALIGNMENTS
Q9XIS5	PRELIMINARY;	PRT; 870 AA.
ID Q9XIS5	Q9XIS5	
AC Q9XIS5	Q9XIS5	
DT 01-NOV-1999	(TREMBLrel. 12, Created)	
DT 01-NOV-1999	(TREMBLrel. 12, Last sequence update)	
DT 01-MAR-2001	(TREMBLrel. 16, Last annotation update)	
DE BRANCHING ENZYME 1	PRECURSOR (EC 2.4.1.18).	
GN KBE1		
OS Phaseolus vulgaris (Kidney bean) (French bean).		
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;		
CC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;		
OC Fabales; Fabaceae; Papilionoideae; Phaseolus.		
OX NCBI_TaxID=3885;		
RN [1]		
RP SEQUENCE FROM N.A.		
RA Mozaki K., Ito H., Matsui H., Honma M.;		
RT "Phaseolus vulgaris L. mRNA for starch branching enzyme 1.";		
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.		
DR EMBL: AB029548; BAA82348.1; -		
DR InterPro: IPR000461; -		
DR Pfam: PF00128; alpha-amylase; 1.		
KW Transl. peptide; Transferase; Glycosyltransferase.		
KW TRANSIT	1	POTENTIAL.
FT SEQUENCE	870 AA; 98890 MW; BDB5C0289B6694EC CRC64;	

Query Match 76.6%; Score 3482.5; DB 10; Length 870;  
Best Local Similarity 73.9%; Pred. No. 1.2e-251;  
Matches 645; Conservative 79; Mismatches 96; Indels 53; Gaps 6;

QY	4	YTIGIRPPCAPLCKSQSTGFHGRRTSCSEFNKFAFSRVSQSKSSSSNNMT	63
DB	3	YTIGIRPP-AYLSLHST-LRGDRRAASLPVFLKNNFSKILAVSSSDSPSSAIA	60
QY	64	ASKRYLDPGRICYSSTQLEAPGVSESOYLTVDESILMDKIYED	113
DB	61	ESDRVLLIPQDHDSASLQDLTEP-----VTSVDANHLDELFWEDBKXNIGRAD	112
QY	114	-----VKSVPAREYSIKIKSKSRSTPPRGRIYDIP	151
DB	113	SYRIEDGLGSSVSPVDVDPARKTSVSGKEVKIPISVPAKGIIPRGAGKIYED	172

QY 152 SLTGROHLDYRYSQYKRLREEDIDYEGSLDAFSGYKFKGFSRSETGITYREMAFGATW 211  
 173 SLAYRHDHDFRGQYKRLREEDIDYEGSLDAFSGYKFKGFSRSETGITYREMAFGATW 232  
 212 AALIGFNNNNPADAATWONECGWIEFLFPNNADGSPPIPHGSRVIRIMDTSGNKDSIP 271  
 233 AALIGFNNNNPADAATWONECGWIEFLFPNNADGSPPIPHGSRVIRIMDTSGNKDSIP 292  
 272 AMIKESVQAGELPYNGIYDPEPEEKYVFNPKPDKSLRIYESHVGSSTPEVINTY 331  
 293 AMIKESVQAGELPYNGIYDPEPEEKYVFNPKPDKSLRIYESHVGSSTPEVINTY 352  
 332 ANFRDVLPRIKKLGAYNAVOIMAOEHSYASFGYHNTFYAASSRFGPDDLSIDKA 391  
 353 ANFRDVLPRIKKLGAYNAVOIMAOEHSYASFGYHNTFYAASSRFGPDDLSIDKA 412  
 392 HELGLVLMIVSHASTNLDGIMNPDGTHYFHSRPGHMMDSRLFNYSMEVIR 451  
 413 HELGLVLMIVSHASTNLDGIMNPDGTHYFHSRPGHMMDSRLFNYSMEVIR 472  
 452 FLISNARWMLDEKDFEPRDGYTSMTYTHGLQVDFGTNYEFGYADVDVATLML 511  
 473 YLLSNARWMLDEKDFEPRDGYTSMTYTHGLQVDFGTNYEFGYADVDVATLML 532  
 512 NDMHGLPEPAVITIGEDVSGMPTVCIPVEDGAVGFDRILHMAVADKRWELLIOKRDDEWK 571  
 533 NDMHGLPEPAVITIGEDVSGMPTVCIPVEDGAVGFDRILHMAVADKRWELLIOKRDDEWK 592  
 572 GDIYHMLTNRWMLDEKCYVAESHDOALVGDKITAFWMLDKMDYDFMALDRSTPLIDRGV 631  
 593 GDIYHMLTNRWMLDEKCYVAESHDOALVGDKITAFWMLDKMDYDFMALDRSTPLIDRGV 652  
 632 ALHNMILITMGLGEGYLNFMNGEFGHPEMIDFPRGDLHPSGKFPVGNYSYDKCRRR 691  
 653 ALHNMILITMGLGEGYLNFMNGEFGHPEMIDFPRGDLHPSGKFPVGNYSYDKCRRR 712  
 692 FDLGNSHRLRYHGMQEPDOALIOHLEAYGFMTSBHOYISKRDEDRITIVERNLVFN 751  
 713 FDLGNSHRLRYHGMQEPDOALIOHLEAYGFMTSBHOYISKRDEDRITIVERNLVFN 772  
 752 FHMNSYSQVRYGCLRGKRYKIVLSDSDPLFSGGRSLSHAEPHSPGWDNDRSPRMV 811  
 773 FHMNSYSQVRYGCLRGKRYKIVLSDSDPLFSGGRSLSHAEPHSPGWDNDRSPRMV 832  
 812 TPCTATVYALVE-----DEVE-----NELEP 833  
 833 APSRTAVYALADLEPAFLDEVEPALADEVER 865

RESULT 2  
 Q41058 PRELIMINARY; PRT: 922 AA.  
 AC Q41058; 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)  
 DE STARCH BRANCHING ENZYME I PRECURSOR.  
 GN SBEI OR SBEI.  
 OS Pisum sativum (Garden pea).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;  
 OC Fabales; Fabaceae; Papilionoideae; Pisum.  
 OC NCBI\_TaxID=3888;  
 RN [1]  
 RE SEQUENCE FROM N. A.  
 RX MEDLINE=5201826; PubMed=7894509;  
 RA Burton R.A., Bewley J.D., Smith A.M., Bhattacharya M.K., Tatge H.,  
 RT "Starch branching enzymes belonging to distinct enzyme families are  
 RT differentially expressed during pea embryo development.";  
 RL Plant J. 7:3-15(1995).  
 DR EMBL: X80009; CAA56319.1; -.

DR Mendel: 16398; Ptsaa; Sbel; 16398.  
 DR InterPro: IPR000461; -  
 DR Pfam: PF00128; alpha-amylase; 1.  
 FT TRANSIT 1 48 POTENTIAL.  
 FT CHAIN 49 922 POTENTIAL.  
 SQ SEQUENCE 922 AA; 105227 MW; 4EDBF9374C6385C8 CRC64;

Query Match 76.3%; Score 3467; DB 10; Length 922;  
 Best Local Similarity 75.6%; Pred. No. 2e-250;  
 Matches 647; Conservative 76; Mismatches 97; Indels 36; Gaps 9;

QY 4 YIISGIRPPCAP-LCKSGSTGFHGRRTSSQLSF--NFKFAFSRRVFSGKSHIESDSSNV 60  
 DB 3 YIISGIRPPCAP-LCKSGSTGFHGRRTSSQLSF--NFKFAFSRRVFSGKSHIESDSSNV 59  
 61 MYTAKRYLPGRIICRYSSSTDLQAPGVSESOVLTVDSLMD----- 107  
 DB 60 TIAESDKVLPEDQNSVSLADQLENPDITSEDAQ--NLEDLAMKQGNKYNDESTSY 116  
 108 KIVEDE-----YKESVPRKTV-SIRKIG-SKPSIIPPGRGORTIDISLT 154  
 DB 117 KEVGEKGSVYSSSLVDYNTDQAKKTSYHSDKRYKDKPIIIPPGGOKIETIDLLQ 176  
 155 GFRHLDYRYSQYKRLREEDIDYEGSLDAFSGYKFKGFSRSETGITYREMAFGATW 214  
 DB 177 AHRHLDYRYSQYKRLREEDIDYEGSLDAFSGYKFKGFSRSETGITYREMAFGATW 236  
 215 IGFNNNNPADAATWONECGWIEFLFPNNADGSPPIPHGSRVIRIMDTSGNKDSIP 274  
 DB 237 VDFNNNNPADAATWONECGWIEFLFPNNADGSPPIPHGSRVIRIMDTSGNKDSIP 292  
 275 KFSVQAGELPYNGIYDPEPEEKYVFNPKPDKSLRIYESHVGSSTPEVINTY 334  
 DB 297 KFSVQAGELPYNGIYDPEPEEKYVFNPKPDKSLRIYESHVGSSTPEVINTY 356  
 335 RDDVLPRIKLGAYNAVOIMAOEHSYASFGYHNTFYAASSRFGPDDLSIDKA 391  
 DB 357 RDDVLPRIKLGAYNAVOIMAOEHSYASFGYHNTFYAASSRFGPDDLSIDKA 412  
 395 GLVLMIVSHASTNLDGIMNPDGTHYFHSRPGHMMDSRLFNYSMEVIR 451  
 DB 417 GLVLMIVSHASTNLDGIMNPDGTHYFHSRPGHMMDSRLFNYSMEVIR 472  
 455 SNARWMLDEKDFEPRDGYTSMTYTHGLQVDFGTNYEFGYADVDVATLML 511  
 DB 477 SNARWMLDEKDFEPRDGYTSMTYTHGLQVDFGTNYEFGYADVDVATLML 532  
 515 IGLPPEAVITIGEDVSGMPTVCIPVEDGAVGFDRILHMAVADKRWELLIOKRDDEWK 571  
 DB 537 IGLPPEAVITIGEDVSGMPTVCIPVEDGAVGFDRILHMAVADKRWELLIOKRDDEWK 592  
 575 VMLTNRWMLDEKCYVAESHDOALVGDKITAFWMLDKMDYDFMALDRSTPLIDRGV 631  
 DB 597 VMLTNRWMLDEKCYVAESHDOALVGDKITAFWMLDKMDYDFMALDRSTPLIDRGV 652  
 635 KMLRLITMGLGEGYLNFMNGEFGHPEMIDFPRGDLHPSGKFPVGNYSYDKCRRR 691  
 DB 657 KMLRLITMGLGEGYLNFMNGEFGHPEMIDFPRGDLHPSGKFPVGNYSYDKCRRR 712  
 695 GSKHLRYHGMQEPDOALIOHLEAYGFMTSBHOYISKRDEDRITIVERNLVFN 751  
 DB 717 GSKHLRYHGMQEPDOALIOHLEAYGFMTSBHOYISKRDEDRITIVERNLVFN 772  
 755 TSSYSQVRYGCLRGKRYKIVLSDSDPLFSGGRSLSHAEPHSPGWDNDRSPRMV 811  
 DB 777 TSSYSQVRYGCLRGKRYKIVLSDSDPLFSGGRSLSHAEPHSPGWDNDRSPRMV 832  
 815 RTAVYALVEDEVE 830  
 DB 837 RTAVYALVEDEVE 851



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RESULT 3
ID 042531 PRELIMINARY; PRT; 800 AA.
AC 042531;
DT 01-NOV-1996 (Tremblrel, 01, Created)
DT 01-NOV-1996 (Tremblrel, 01, last sequence update)
DT 01-MAY-2000 (Tremblrel, 13, last annotation update)
DE STARCH BRANCHING ENZYME CLASS II (EC 2.4.1.18) (1,4-ALPHA-GLUCAN
DE BRANCHING ENZYME) (GLYCOGEN BRANCHING ENZYME) (AMYLO-(1,4 TO
DE 1,6) TRANSGLUCOSIDASE) (AMYLO-(1,4-1,6)-TRANSGLUCOSYLASE) (FRAGMENT).
DE SBE1 OR SBE2-2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsids.
OC NCBI_taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ECOTYPE COLUMBIA; TISSUE=HYPOCOTYL;
RX MEDLINE=96197401; PubMed=8616246;
RA Fisher D.K., Gao M., Kim K.N., Boyer C.D., Gullinan M.J.;
RT "Two closely related cDNAs encoding starch branching enzyme from
RT Arabidopsis thaliana."
RL Plant Mol. Biol. 30:97-108(1996).
CC -1- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF
CC GLYCOGEN.
EMBL: U22428; AAB03100.1; -;
DR Mendel; 16401; Arabid; Sbel; 16401.
DR InterPro: IPR000461; -;
DR Pfam: PF00128; alpha-amyrase; 1.
FT Transferase; Glycosyltransferase.
FT NON_TER 1
SQ SEQUENCE 800 AA; 92098 MW; 8D47E9404B03258 CRC64;

Query Match 74.5%; Score 3384.5; DB 10; Length 800;
Best Local Similarity 75.5%; Pred. No. 2.3e-244;
Matches 619; Conservative 80; Mismatches 86; Indels 35; Gaps 8;

QY 12 PCAPLCKSGSTGHHYRTSSCLSFNFK-AFSRRVFGSKSHESDSNVMTASKRYLP 70
DB 11 PSRPL-----NTGFNA---GNSLSEFFKKHPLSRIFAGKQSAEPDSSQAISAEKVL 62
QY 71 DGRLECYSSSTQLEAPGVYSEE-----SOVLVDVSLIMDKIYEDVKNESVPMRETVS 126
DB 63 -----VPDNLDDPPRGFSQIF-DLESQYME---YTEAVRTEDQTMN---V 100
QY 127 IRRIGSKPRSIPPRGGRORIYDIPSLTGFROHLDIRYSQYKRLREEDIKYEGSLDAFSR 186
DB 101 VKERGVKPRIVPPGDKKIYEIDPMLRTYNNHLDYRQYKRLREEDIKYEGSLDAFSR 160
QY 187 GYKRGFSSESGITRYRENAFGATMAALIGDPNNMNPADVMTQNEGCVWEIFLPNNADG 246
DB 161 GYKLGFSRSDAGITRYRENAFGAKAASLIGDPNNMNSNADIMTRNEFGVWEIFLPNNADG 220
QY 247 SPPIPGHSVKIRMDTPSGNKSIPAWIKFSYQAPGELPYNGIYDPEEEKYVFKRNP 306
DB 221 SPPIPGHSVKIRMDTPSGIKSIPAWIKFSYQAPGELPYNGIYDPEEEKYVFKRNP 280
QY 307 KKRKSLRIEESHVAGMSSTPEVINTYANFRDVLPRIKRLGYNANVQALMIOHSHSYASFGY 366
DB 281 KKRKSLRIEESHVAGMSSTPEVINTYANFRDVLPRIKRLGYNANVQALMIOHSHSYASFGY 340
QY 367 HTYNFNAASRGTPDDKSLIDKAHEGLGLVLMIVYSHASTNTLDGLNFGDGDHAYF 426
DB 341 HTYNFNAASRGTPDEKSLIDKAHEGLGLVLMIVYSHASTNTLDGLNFGDGDHAYF 400
QY 427 HSGPRGHMMWMDSLFNTGSMVEVLFRLSLNARMWLDKFKFGFPGDGTSMYTHHGLSY 486
DB 401 HSGPRGHMMWMDSLFNTGSMVEVLFRLSLNARMWLDKFKFGFPGDGTSMYTHHGLSY 460
QY 487 DPTGNVNEFGIATVDVAVYVLMILNDMIGHLPFAVITIGDVGSMPTVCIPEVDGGVGF 546

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DB 461 GFTGNVTEYFGLIEDVDVAVNTLMVNMKIHGLYPEALITVGEDVSGMFTFCIPVQDGGVGF 520
QY 547 DYRLHMAVADKWVELIQRDEDMKMGDIVHMLTNRRLKRCVSAESHDQALVGDKTIAF 606
DB 521 DYRLHMAVADKWIELMKRDEDMQMGDIYVLTTRRRESEKISIAESHDQALVGDKTIAF 580
QY 607 WLMQDMVDFMAALRPSRPLDRGVLAHKMIRLITMGLSGEGLINTMGNEFGHPENIDPP 666
DB 561 WLMQDMVDFMAVDPSTPLDRGIALHKMIRLITMGLSGEGLINTMGNEFGHPENIDPP 640
QY 667 RGDLLPSGKFPVGNNSYDCKRRRFDLGNLSKHLRYGMEQFOALQHEAVGEMTSEH 726
DB 641 RGEORLSGVSITPCNNNSYDCKRRRFDLGDADYLRYGLOEFOAQHLEPNTGFTSEH 700
QY 727 QYISKDEDRKIYFEGNGLVFNFNHWTSSYSYDVRVCLPKPKYKIVLSDDPPLFGGFG 786
DB 701 QYISKDEADRVIVFERGDIIVFENFHWTSYFDYRIGCSKPKYKIVLSDDPPLFGGFG 760
QY 787 RLSDHAHFSPGFWYDNRPSFWYPCRTAVVYALVEDE 826
DB 761 RLSDKAFFYTDGLYDERPCSFMYVAPCRVAVYALANHD 800

RESULT 4
ID 09LZS3 PRELIMINARY; PRT; 805 AA.
AC 09LZS3;
DT 01-OCT-2000 (Tremblrel, 15, Created)
DT 01-OCT-2000 (Tremblrel, 15, last sequence update)
DT 01-OCT-2000 (Tremblrel, 15, last annotation update)
DE 1,4-ALPHA-GLUCAN BRANCHING ENZYME PROTEIN SOFORM SBE2.2 PRECURSOR.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsids.
OC NCBI_taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Pohl T., Welzenegger T., Bancroft I., Mewes H.W., Rudd S.,
RA Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project.
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
EMBL: AL162506; CAB82930.1; -;
SQ SEQUENCE 805 AA; 92591 MW; 7CE130BD9C4941D0 CRC64;

Query Match 74.5%; Score 3384.5; DB 10; Length 805;
Best Local Similarity 75.5%; Pred. No. 2.3e-244;
Matches 619; Conservative 80; Mismatches 86; Indels 35; Gaps 8;

QY 12 PCAPLCKSGSTGHHYRTSSCLSFNFK-AFSRRVFGSKSHESDSNVMTASKRYLP 70
DB 16 PSRPL-----NTGFNA---GNSLSEFFKKHPLSRIFAGKQSAEPDSSQAISAEKVL 67
QY 71 DGRLECYSSSTQLEAPGVYSEE-----SOVLVDVSLIMDKIYEDVKNESVPMRETVS 126
DB 68 -----VPDNLDDPPRGFSQIF-DLESQYME---YTEAVRTEDQTMN---V 105
QY 127 IRRIGSKPRSIPPRGGRORIYDIPSLTGFROHLDIRYSQYKRLREEDIKYEGSLDAFSR 186
DB 106 VKERGVKPRIVPPGDKKIYEIDPMLRTYNNHLDYRQYKRLREEDIKYEGSLDAFSR 165
QY 187 GYKRGFSSESGITRYRENAFGATMAALIGDPNNMNPADVMTQNEGCVWEIFLPNNADG 246
DB 166 GYKLGFSRSDAGITRYRENAFGAKAASLIGDPNNMNSNADIMTRNEFGVWEIFLPNNADG 225
QY 247 SPPIPGHSVKIRMDTPSGNKSIPAWIKFSYQAPGELPYNGIYDPEEEKYVFKRNP 306
DB 221 SPPIPGHSVKIRMDTPSGIKSIPAWIKFSYQAPGELPYNGIYDPEEEKYVFKRNP 280

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Db 226 SPATPGSRVIRMDTPSGIKDISIPAMIKFSVQAPCEIPENGIIYDPEEKKYVFKHPQ 285
Oy 307 KRPKSLRIYSEHVGMSSTEVYINTYANFRDVLPRIKKIGYNAVOLMAIOEHSYVAFSG 366
Db 286 KRPKSLRIYEAHVAGSSTEVYNTYANFRDVLPRIKKIGYNAVOLMAIOEHSYVAFSG 345
Oy 367 HTNRYAASRSFGPEDDLSLIDRAHEGLGLVLMIDYHSAHSTNTDGLNMFPGDTGHYF 426
Db 346 HTNRYAASRSFGPEDDLSLIDRAHEGLGLVLMIDYHSAHSTNTDGLNMFPGDTGHYF 405
Oy 427 HSGPRGHMMMDSRLEFNGSWEVLEFLSNARWMLDEKDFGFRFDDVTSMYTHHGLQY 486
Db 406 HSGPRGHMMMDSRLEFNGSWEVLEFLSNARWMLDEKDFGFRFDDVTSMYTHHGLQY 465
Oy 487 DETGNYNEFGYATDVDAVYVYLMIDMLNMIHGLFPEAVTIGEDVSGMPTVCIPVEDGSGVF 546
Db 466 DETGNYNEFGYATDVDAVYVYLMIDMLNMIHGLFPEAVTIGEDVSGMPTVCIPVEDGSGVF 525
Oy 547 DYLHNAVADKRVETIIOKREDEMGKGLVHMLTNRNMLEKCVSAEASHDQALVADKTIAT 606
Db 526 DYLHNAVADKRVETIIOKREDEMGKGLVHMLTNRNMLEKCVSAEASHDQALVADKTIAT 585
Oy 607 WLMKDMYDPMALDRPSTPLIDRGVALHMKMRLITMGIGSGYLNFMGNERGHEWIDFP 666
Db 586 WLMKDMYDPMALDRPSTPLIDRGVALHMKMRLITMGIGSGYLNFMGNERGHEWIDFP 645
Oy 667 RGDHLPSKFPYNNYSTDCKRRFDLGDADYLRKRGLOEFDQAMQHLNENYGFMTSEH 726
Db 646 RGDHLPSKFPYNNYSTDCKRRFDLGDADYLRKRGLOEFDQAMQHLNENYGFMTSEH 705
Oy 727 QYTSRDEDRILVIERKGLVYVFNHMTSSSDYRNGCLPKGKXKTYLDSDDDLFGGFG 786
Db 706 QYTSRDEDRILVIERKGLVYVFNHMTSSSDYRNGCLPKGKXKTYLDSDDDLFGGFG 765
Oy 787 RLSHDAEHSFEGWYDNRPSFNVYTPCCTAVVYALVEDE 826
Db 766 RLSHDAEHSFEGWYDNRPSFNVYTPCCTAVVYALVEDE 805
RESULT 5
OYXGAG PRELIMINARY: PRT: 878 AA.
ID OYXGAG;
AC 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, last annotation update)
DE STARCH BRANCHING ENZYME II PRECURSOR (EC 2.4.1.18).
SBE II.
OS Solanum tuberosum (Potato).
OC Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta:
OC Magnoliophyta: eudicotyledons: core eudicots: Asteridae: euasterids I:
OC Solanales: Solanaceae: Solanum.
OX NCBI_TaxID=4113;
RN SEQUENCE FROM N.A.
RC STRAIN=CV. DESPRE.
RA JOHNSON S.A., Schwall G.P., Westcott R.J., Sidebottom C.M., Debet M.,
RA Gidley M.J., Jelicic R., Safford R.
RT "A minor form of starch branching enzyme in potato (Solanum tuberosum
RT L.) tubers has a major effect on starch structure, cloning and
RT characterization of multiple forms of SBE II."
RL Submitted (Oct-1998) to the EMBL/GenBank/DBD databases.
DR EMBL: AJ011888; CAB40746.1; -.
DR InterPro: IPR000461; -.
DR Pfam: PF00128; alpha-amylase; 1.
DR Transit peptide; Transferase; Glycosyltransferase.
FT TRANSIT 1 48 POTENTIAL.
FT CHAIN 49 878 STARCH BRANCHING ENZYME II.
SQ SEQUENCE 878 AA: 100411 MW: 558186A39DF8F53 CRC64:
Query Match 74.4%; Score 3381.5; DB 10; Length 878;
Best Local Similarity 71.4%; Pred. No. 4.5e-244;

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Matches 617; Conservative 95; Mismatches 117; Indels 35; Gaps 5;
Oy 4 YTGISGFPAP-LCKSQSTGFHGYRTSCLSFNFKAEFSRVSGKSHSISNNVY 62
Db 3 YTGISGFPAP-LCKSQSTGFHGYRTSCLSFNFKAEFSRVSGKSHSISNNVY 62
Oy 63 TASKRVLDG-RICVSSSTDDLEAPGVSESOVLVEESLIMDQ-----KIVDEV--- 114
Db 63 TASKRVLDG-RICVSSSTDDLEAPGVSESOVLVEESLIMDQ-----KIVDEV--- 114
Oy 63 AASGKVLVPGIGSSSSSSSDQPEFAETSPENSASPADVDSSTMEHASOKITENDVPS 122
Db 63 AASGKVLVPGIGSSSSSSSDQPEFAETSPENSASPADVDSSTMEHASOKITENDVPS 122
Oy 115 -----NKSVMRETVSIRKGS-----KPSIIPPGRGORID 148
Db 123 SDLGVSVELDFPASTLOQEGKLEESKTLNTESEPTIDESDRIRREGIIPPCGKIVE 182
Oy 149 IDPSLTGFRHLDRYQYKRLREIDYEGSLDAPSRGYEKGRFSEGTITREMAFG 208
Db 183 IDPLLTNRHLDYRISQYKRLRAIDYEGSLDAPSRGYEKGRFSEGTITREMAFG 242
Oy 209 ATWALIDENNNBNADVMTQNECYWEIPIPNADGSPPIHSGSVKTRMDTPSGND 268
Db 243 AOSAAALIDFNMMNADFMTRNEFGWELIPNNVDSFALHSGSVKTRMDTPSGND 302
Oy 269 SIPAMIKFSVQAPGELPYNGIYDPEEKKYVFNKPKRPSIRIYSEHVGMSSTEVY 328
Db 303 SIPAMIKFSVQAPGELPYNGIYDPEEKKYVFNKPKRPSIRIYSEHVGMSSTEVY 362
Oy 329 NTYANFRDVLPRIKKIGYNAVOLMAIOEHSYVAFSGHYTNFYAASRSFGPEDDLSL 388
Db 363 NSYVNRDEVLPRIKKIGYNAVOLMAIOEHSYVAFSGHYTNFYAASRSFGPEDDLSL 422
Oy 389 DRAHEGLGLVLMIDYHSAHSTNTDGLNMFPGDTGHYHSGPRGHMMMDSRLEFNGS 448
Db 423 DRAHEGLGLVLMIDYHSAHSTNTDGLNMFPGDTGHYHSGPRGHMMMDSRLEFNGS 482
Oy 449 VLEFLSNARWMLDEKDFGFRFDDVTSMYTHHGLQYDTGNTNEXFGATLVDAVYV 508
Db 483 VLEFLSNARWMLDEKDFGFRFDDVTSMYTHHGLQYDTGNTNEXFGATLVDAVYV 542
Oy 509 MLNDMIMHGLFPEAVTIGEDVSGMPTVCIPVEDGSGVGFYRLHNAVADKVEIIOKRE 568
Db 543 MLNDMIMHGLFPEAVTIGEDVSGMPTVCIPVEDGSGVGFYRLHNAVADKVEIIOKRE 602
Oy 569 WKMGDIYHMLTNRNMLEKCVSAEASHDQALVADKTIATWLMKDMYDPMALDRPSTPL 628
Db 603 WKMGDIYHMLTNRNMLEKCVSAEASHDQALVADKTIATWLMKDMYDPMALDRPSTPL 662
Oy 629 RGVALKMRLITMGIGSGYLNFMGNERGHEWIDFPDGLHLPSGKFPYNNYSTDCK 688
Db 663 RGVALKMRLITMGIGSGYLNFMGNERGHEWIDFPDGLHLPSGKFPYNNYSTDCK 722
Oy 689 RRRFDLGNKHLRHHMOEFDQALHLEAVGFMPTSEHOYTSRDEDRILVIERKGLV 748
Db 723 RRRFDLGNKHLRHHMOEFDQALHLEAVGFMPTSEHOYTSRDEDRILVIERKGLV 782
Oy 749 VNFHMTSSYDVRGCLPKGKXKTYLDSDDDLFGGFRGLSHDAEHSFEGWYDNRPS 808
Db 783 VNFHMTSSYDVRGCLPKGKXKTYLDSDDDLFGGFRGLSHDAEHSFEGWYDNRPS 842
Oy 809 MYTTPCCTAVVYALVEDEENLE 832
Db 843 MYTTPCCTAVVYALVEDEENLE 866
RESULT 6
ID O23647 PRELIMINARY: PRT: 858 AA.
AC O23647;
DT 01-JUN-1998 (Tremblrel. 05, Created)
DT 01-JUN-1998 (Tremblrel. 05, last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, last annotation update)
DE STARCH BRANCHING ENZYME II (EC 2.4.1.18) (1,4-ALPHA-GLUCAN BRANCHING
DE ENZYME) (GLYCOGEN BRANCHING ENZYME) (AMYLO-(1,4-1,6)-TRANSGLUCOSYLASE).
DE 1,6)TRANSGLUCOSYLASE) (AMYLO-(1,4-1,6)-TRANSGLUCOSYLASE).

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GN SBE1 OR SBE2.1 OR F1011.2.  
 OC Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids II;  
 OC Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV, COLUMBIA;  
 RA Khoshnoodi J.;  
 RL Thesis (1997), Swedish University of Agricultural Sciences, Sweden.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV, COLUMBIA;  
 RA Lin X., Kaul S., Sneha T.P., Fujii C.Y., Shen M., Vanaken S.E.,  
 RA Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.,  
 RA Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,  
 RA Fraser C.M., Venter J.C.;  
 RT "Arabidopsis thaliana chromosome II BAC F1011 genomic sequence,"  
 RT Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF  
 CC GLUCOGEN.  
 DR EMBL; AJ000497; CAA04134.1; -  
 DR EMBL; AC006919; AAD24644.1; -  
 DR Mendel; 24099; Arach: sbe1; 24099.  
 DR InterPro: IPR000461; -  
 DR Pfam: PF00128; alpha-amylase; 1.  
 DR Trasnferase; Glycosyltransferase.  
 KM SEQUENCE 858 AA; 97659 MW; E1D61C0C21D456F1 CRC64;  
 SQ  
 Query Match 74.2%; Score 3373; DB 10; Length 858;  
 Best Local Similarity 72.0%; Pred. No. 1.9e-243;  
 Matches 617; Conservative 104; Mismatches 102; Indels 34; Gaps 6;  
 OY 4 YTTGIRPCAPLCKSOSTGFHGR--RTSCLSFNKE--AFSRVSGKSHESDSS 58  
 DB 3 YTTGIRPCAPLCKSOSTGFHGR--RTSCLSFNKE--AFSRVSGKSHESDSS 58  
 OY 59 NMYATLAKRVLPRGRLECYSSSTDLLEAPGVSESOVLTVESLIMDKIVEDEVNKS 118  
 DB 63 SLATTYASEK-LRHQSDSSSSASDQVSDRYVDDPQVGLNVD-----VQKTEAGET 114  
 OY 119 VPMREYSIRKIGS-----KPSIPRPGRGORTDIPSLTGFROHL 160  
 DB 115 ETLDTGTSALSTSGISYKEDFAKMSHVQEVQGRKIPPGGKRTYDIDPLNSHRHL 174  
 OY 161 DYRSQYKRLREIDYKESGLAFSGRYEKFGRSSEGTITREMAPGATMALIGDFNN 220  
 DB 175 DYRGQYKRLREIDYKESGLAFSGRYEKFGRSSEGTITREMAPGATMALIGDFNN 234  
 OY 221 WNPNAVDMQNEGVWEIPLPNADSPPIPHGSRKRTIMDTPSGKSDIPAMIKFSVOA 280  
 DB 235 WNAKSDVMAANDGVWEIPLPNADSPPIPHGSRKRTIMDTPSGKSDIPAMIKFSVOA 294  
 OY 281 PGLPFGNYIYDPEPEKVFVKNPQKRPKSLRTIESHVGMSSTPVTINTANFRDVL 340  
 DB 295 PGLPFGNYIYDPEPEKVFVKNPQKRPKSLRTIESHVGMSSTPVTINTANFRDVL 354  
 OY 341 RIKKLIYNAVQMAIOEHSYVAFSGYHVTNFEYAASSRGTDPDLKSLDKAKHELGLVLM 400  
 DB 355 RIKKLIYNAVQMAIOEHSYVAFSGYHVTNFEYAASSRGTDPDLKSLDKAKHELGLVLM 414  
 OY 401 DIYHSHASTNTDGLNMPGTDGHHFHSRPGHMMMDSLFNYSWVLYLFLSNARW 460  
 DB 415 DIYHSHASTNTDGLNMPGTDGHHFHSRPGHMMMDSLFNYSWVLYLFLSNARW 474  
 OY 461 LDEYKDFGRFDGVTSMYTHGLQVDFGNTNEFGYATVDVAVYUMLNDMIGL 520  
 DB 475 LDEYKDFGRFDGVTSMYTHGLQVDFGNTNEFGYATVDVAVYUMLNDMIGL 534  
 OY 521 EANTIGEDSVGMPYVCIPEDEGCVFDRILAAVADKVEIIOKREDEKMGDIVHMLTN 580  
 DB 535 EALVGEDVSGMPARFVPEDEGCVFDRILAAVADKVEIIOKREDEKMGDIVHMLTN 594

DB 535 EALVGEDVSGMPARFVPEDEGCVFDRILAAVADKVEIIOKREDEKMGDIVHMLTN 594  
 OY 581 RRMLEKCVSYAESDQALVGKTLTAFLMDKMDYFALDRPSTPLIDRGVALHKMIRL 640  
 DB 595 RRMLEKCVSYAESDQALVGKTLTAFLMDKMDYFALDRPSTPLIDRGVALHKMIRL 654  
 OY 641 TMGLGEGYLNMGNENEPHGPMDLPLSGKRVPPNNNSYDKCRREFLGSKHL 700  
 DB 655 TMGLGEGYLNMGNENEPHGPMDLPLSGKRVPPNNNSYDKCRREFLGSKHL 714  
 OY 701 RYHGMQEPDQALQHLLEAVYGFMTSEHGYISRKDERRIYFERGNLVFNFHMTSSYS 760  
 DB 715 RYHGMQEPDQALQHLLEAVYGFMTSEHGYISRKDERRIYFERGNLVFNFHMTSSYS 774  
 OY 761 YRIGSVGKTKYIVLDSDPLFGFGLSHDAHEFSEGYDNRPSEMYTTPCRAVY 820  
 DB 775 YRIGSVGKTKYIVLDSDPLFGFGLSHDAHEFSEGYDNRPSEMYTTPCRAVY 834  
 OY 821 ALVEDEVENE--LEPV 834  
 DB 835 AAVDDDDDERSSLVPI 851  
 RESULT 7  
 ID 09XGA5 PRELIMINARY; PRT; 871 AA.  
 AC 09XGA5;  
 DT 01-NOV-1999 (TREMURel. 12, Created)  
 DT 01-NOV-1999 (TREMURel. 12, Last sequence update)  
 DT 01-MAR-2001 (TREMURel. 16, Last annotation update)  
 DE STARCH BRANCHING ENZYME II PRECURSOR (EC 2.4.1.18).  
 GN SBE II.  
 OS Solanum tuberosum (Potato).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;  
 CC Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4113;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV, DESIREE;  
 RA Jobling S.A., Schwall G.P., Westcott R.J., Sidebottom C.M., Debet M.,  
 RA Gidley M.J., Jeffcoat R., Safford R.;  
 RT "A minor form of starch branching enzyme in potato (Solanum tuberosum  
 RT L.) tubers has a major effect on starch structure; cloning and  
 RT characterisation of multiple forms of SBE II.";  
 RT Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ011885; CAB40743.1; -  
 DR InterPro: IPR000461; -  
 DR Pfam: PF00128; alpha-amylase; 1.  
 DR Trasnferase; Glycosyltransferase.  
 KM TRANSIT PEPTIDE; TRANSFERASE; POTENTIAL.  
 FT CHAIN 1 48  
 FT 49 871 STARCH BRANCHING ENZYME II.  
 SQ SEQUENCE 871 AA; 99417 MW; 6F1F094247676938 CRC64;  
 Query Match 73.9%; Score 3360; DB 10; Length 871;  
 Best Local Similarity 71.4%; Pred. No. 1.8e-242;  
 Matches 619; Conservative 94; Mismatches 118; Indels 36; Gaps 6;  
 OY 4 YTTGIRPCAP-LCKSOSTGFHGRRTSSCLSFNKEAFKAFSRVSGKSHESDSSNMY 62  
 DB 3 YTTGIRPCAP-LCKSOSTGFHGRRTSSCLSFNKEAFKAFSRVSGKSHESDSSNMY 62  
 OY 63 TASKRVL-PDGRITCYSSSTDLLEAPGVSESOVLTVESLIMD---RTVEDEV--- 114  
 DB 63 TASKRVL-PDGRITCYSSSTDLLEAPGVSESOVLTVESLIMD---RTVEDEV--- 122  
 OY 115 -----KKEVPAREVYSIRKIGS-----KPSIPRPGRGORTYD 148  
 DB 123 SDLTGVEELDASSLQLOEGGKLEESKTLNLTSETIIDESDRIRERGIPTPGIGQYIE 182  
 OY 149 IDPSLTGFRQHLQDYRSQYKRLREIDYKESGLAFSGRYEKFGRSSEGTITREMAPG 208  
 DB 149 IDPSLTGFRQHLQDYRSQYKRLREIDYKESGLAFSGRYEKFGRSSEGTITREMAPG 208

Db 183 IDPLLTNYKOHLDYRYSOYKRLREAIIDRYEGGLEAFSGYKMGFTTSATGITYREMAPG 242  
 QY 209 ATWALIDGFNNMNPADWMTQNECGWEIFLPNNADSPPIPHGSRVYKIRMDTPSGNKD 268  
 Db 243 AQSALLIGFNNMNDADIMTRNEFGWEIFLPNNVDGSPAIPIHSGSRVYKIRMDTPSGNKD 302  
 QY 269 SIPAWIKESVOAAGELPYNIGIYDPEPEEKYKFNOPKPKRSKIRIYESHVGMSSTPEVI 328  
 Db 303 SIPAWIKESVOAAGELPYNIGIYDPEPEEKYKFNOPKPKRSKIRIYESHVGMSSTPEVI 362  
 QY 329 NITYANFRDYLPRIRIKLGNAYOALIOHSHYASFGYHVTNFEYAASSFGPTDPLKSI 388  
 Db 363 NSIVNFRDYLPRIRIKLGNAYOALIOHSHYASFGYHVTNFEYAASSFGPTDPLKSI 422  
 QY 389 DKAHELGLVLMIDYHSHASTYTLGLNMFDOGTGHHFSGRGHHMMWDSRLFYSGME 448  
 Db 423 DKAHELGLVLMIDYHSHASTYTLGLNMFDOGTGHHFSGRGHHMMWDSRLFYSGME 482  
 QY 449 VLRFLLSNARWMLDEYKFGDFRFGVTSMTYTHHGLQVDFGNTNNEYRGATVDVAVYL 508  
 Db 483 VLRFLLSNARWMLDEYKFGDFRFGVTSMTYTHHGLQVDFGNTNNEYRGATVDVAVYL 542  
 QY 509 MLNDMIDHGLFPEAVTIGEDVSGMPTVCIPVEDGSGVGFYRLHMAVADKWEI10KRD 568  
 Db 543 MLNDMIDHGLFPEAVTIGEDVSGMPTVCIPVEDGSGVGFYRLHMAVADKWEI10KRD 602  
 QY 569 WKMGDIYHMLTNRWLEKCVSAESHDQALVGDKTAFWLMKDMDYDFMALDRPSTPLID 628  
 Db 603 WKMGDIYHMLTNRWLEKCVSAESHDQALVGDKTAFWLMKDMDYDFMALDRPSTPLID 662  
 QY 629 RGVALKHMTILTMGLGEGEYLNFMNGEFGHEWIDFPGDHLPSGKVPNGNYSYDKC 688  
 Db 663 RGVALKHMTILTMGLGEGEYLNFMNGEFGHEWIDFPGDHLPSGKVPNGNYSYDKC 722  
 QY 689 RRRFDLGNKHLRYHGMOFDOALIOHLEAYGFMSEHVISKRDSDRIYERGNLVF 748  
 Db 723 RRRFDLGNKHLRYHGMOFDOALIOHLEAYGFMSEHVISKRDSDRIYERGNLVF 782  
 QY 749 VFNFWHTSSYSDRYVGLKPKKRYKIVLSDPDLFGGFGSLSHDAHEPFGWDMNPRSF 808  
 Db 783 VFNFWHTSSYSDRYVGLKPKKRYKIVLSDPDLFGGFGSLSHDAHEPFGWDMNPRSF 842  
 QY 809 MYTPCRTAVVAVYALVLED-EVEENLEPY 834  
 Db 843 MYTPCRTAVVAVYALVLED-EVEENLEPY 869

RESULT 8  
 Q9XGAB PRELIMINARY; PRT; 882 AA.  
 AC Q9XGAB;  
 DT 01-NOV-1999 (Tremblrel. 12, Created)  
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
 DE STARCH BRANCHING ENZYME II PRECURSOR (EC 2.4.1.18).  
 GN SBE II.  
 OS Solanum tuberosum (potato).  
 OC Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta;  
 OC Magnoliophyta: eudicotyledons: core eudicots: Asteridae: euasterids I;  
 OC Solanales: Solanaceae: Solanum.  
 OC NCBI\_TaxID=4113;  
 RX [1]  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV DESIREE;  
 RA JODLING S.A., Schwab, G.P., Westcott R.J., Sidebottom C.M., Debet M.,  
 RA Gidley M.J., Jeffcoat R., Safford R.;  
 RT "A minor form of starch branching enzyme in potato (Solanum tuberosum  
 RT L.) tubers has a major effect on starch structure: cloning and  
 RT characterisation of multiple forms of SBE II.\*";  
 RL Submitted (Oct-1998) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AJ011890; CAB40748.1; -;  
 DR InterPro; IPR000461; -;  
 DR Pfam; PF00128; alpha-amylase; 1.

KW Transit peptide: Transferase; Glycosyltransferase.  
 FT TRANSIT 49 882 POTENTIAL.  
 FT CHAIN 49 STARCH BRANCHING ENZYME II.  
 SO SEQUENCE 882 AA; 100863 MW; FB50F9AF825EB87 CRC64;

Query Match 73.8%; Score 3356; DB 10; Length 882;  
 Best Local Similarity 70.9%; Pred. No. 3.6e-242;  
 Matches 617; Conservative 96; Mismatches 119; Indels 38; Gaps 6;

4 YTGIRFPAC-LCKSOSTGFHGYRTSSCLSPNFKAFSRVYSGKSHESDSSNMY 62  
 Db 3 YTGIRFPAC-LCKSOSTGFHGYRTSSCLSPNFKAFSRVYSGKSHESDSSNMY 62  
 QY 63 TASKRVL-PDGRLECYSSSTDOLEAPCTVSESOVLTVESLIMD---KIVZDEY--- 114  
 Db 63 TASKRVL-PDGRLECYSSSTDOLEAPCTVSESOVLTVESLIMD---KIVZDEY--- 114  
 QY 115 -----NKESVPMRETVSIRKIGS-----KPSIPPGRQRIYD 148  
 Db 123 SDLGVELEDFASSILOEGCKLEESKTLNTSEETIIDESDRIRERGIIPPGLGKIYE 182  
 QY 149 IDPLTNYKOHLDYRYSOYKRLREAIIDRYEGGLEAFSGYKMGFTTSATGITYREMAPG 208  
 Db 183 IDPLTNYKOHLDYRYSOYKRLREAIIDRYEGGLEAFSGYKMGFTTSATGITYREMAPG 242  
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 QY 269 SIPAWIKESVOAAGELPYNIGIYDPEPEEKYKFNOPKPKRSKIRIYESHVGMSSTPEVI 328  
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 Db 483 VLRFLLSNARWMLDEYKFGDFRFGVTSMTYTHHGLQVDFGNTNNEYRGATVDVAVYL 542  
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 QY 569 WKMGDIYHMLTNRWLEKCVSAESHDQALVGDKTAFWLMKDMDYDFMALDRPSTPLID 628  
 Db 603 WKMGDIYHMLTNRWLEKCVSAESHDQALVGDKTAFWLMKDMDYDFMALDRPSTPLID 662  
 QY 629 RGVALKHMTILTMGLGEGEYLNFMNGEFGHEWIDFPGDHLPSGKVPNGNYSYDKC 688  
 Db 663 RGVALKHMTILTMGLGEGEYLNFMNGEFGHEWIDFPGDHLPSGKVPNGNYSYDKC 722  
 QY 689 RRRFDLGNKHLRYHGMOFDOALIOHLEAYGFMSEHVISKRDSDRIYERGNLVF 748  
 Db 723 RRRFDLGNKHLRYHGMOFDOALIOHLEAYGFMSEHVISKRDSDRIYERGNLVF 782  
 QY 749 VFNFWHTSSYSDRYVGLKPKKRYKIVLSDPDLFGGFGSLSHDAHEPFGWDMNPRSF 808  
 Db 783 VFNFWHTSSYSDRYVGLKPKKRYKIVLSDPDLFGGFGSLSHDAHEPFGWDMNPRSF 842  
 QY 809 MYTPCRTAVVAVYALVLED-EVEENLEPY 835  
 Db 843 MYTPCRTAVVAVYALVLED-EVEENLEPY 872

RESULT 9  
 049553



Db 181 GTRSATGATYREMAPGASALIDGFNNMADIMTRNEFGWELFPNNVDSPAIP 240  
 QY 252 HGSRAKIMNDPPSGNKSIPAMIKFSVOAPGELPANGIYYPPEBEKVFKNPOPKRKS 311  
 Db 241 HGSRAKIMNDPPSGYKDSIPAMINVSIGLPDEIPYNGIYYPPEBERIYFQHPRPKRKS 300  
 QY 312 LRIYSHGMSSTPEVITFANFRDVLPRIKKIGYNAVOMALIOESHYASFGYHTNF 371  
 Db 301 LRIYSHGMSSTPEKINSYNFREVPRIKKGYNALQIMAOESHYASFGYHTNF 360  
 QY 372 YAAASRETPDRIKLIKAEHIGLVMDIVHSHASTNTDGLMPDGTGCHPESGR 431  
 Db 361 FAPSRFGIPDGLKLIKAEHIGLVMDIVHSHASTNTDGLMPDGTGCHPESGR 420  
 QY 432 GHMMWDRLENYGSEWELRELLSNARWMLDDEKFGFREDGVTSMYTHGLVDFTGN 491  
 Db 421 GHMMWDRLENYGSEWELRELLSNARWMLDDEKFGFREDGVTSMYTHGLVDFTGN 480  
 QY 492 YNEFYATDVAVYVIMLMDMTHGLEPFAVTTIGEDVSGMPTVCIPVEDGSGVEDYRLH 551  
 Db 481 YNEFYATDVAVYVIMLMDMTHGLEPFAVTTIGEDVSGMPTVCIPVEDGSGVEDYRLH 540  
 QY 552 MAVADKWEIIOKREDKMGDIYHMLNRRWLEKCVSYASHOQALVGDKTIFWIMDK 611  
 Db 541 MAVADKWEIIOKREDKMGDIYHMLNRRWLEKCVSYASHOQALVGDKTIFWIMDK 600  
 QY 612 DMYDENALDRPSTPLIDGVALHMKIRLITMGLGEGYLNMGNEFGHPEWIDPREGDLH 671  
 Db 601 DMYDENALDRPSTPLIDGVALHMKIRLITMGLGEGYLNMGNEFGHPEWIDPREGDLH 660  
 QY 672 LPSGFVGNVSYKCRRRFDIGSKLRYHGMQEPFOALIOHEAVGEMTSEHOYSR 731  
 Db 661 LPSGFVGNVSYKCRRRFDIGSKLRYHGMQEPFOALIOHEAVGEMTSEHOYSR 720  
 QY 732 KDERRITVFERGNLYVFENFHTSSYSDRYGCLPKGKYITVDSDDLPGGGRSLHD 791  
 Db 721 KDERRITVFERGNLYVFENFHTSSYSDRYGCLPKGKYITVDSDDLPGGGRSLHD 780  
 QY 792 AEHFEFGVGNVSYKCRRRFDIGSKLRYHGMQEPFOALIOHEAVGEMTSEHOYSR 835  
 Db 781 AEHFEFGVGNVSYKCRRRFDIGSKLRYHGMQEPFOALIOHEAVGEMTSEHOYSR 826

RESULT 11  
 Q42526 PRELIMINARY; PRT; 854 AA.  
 AC 042526;  
 DT 01-NOV-1996 (TREMUREL. 01, Created)  
 DT 01-NOV-1996 (TREMUREL. 01, Last sequence update)  
 DT 01-MAY-2000 (TREMUREL. 13, Last annotation update)  
 DE STRACH BRANCHING ENZYME CLASS II (EC 2.4.1.18) (1,4-ALPHA-GLUCAN  
 BRANCHING ENZYME) (GLYCOGEN BRANCHING ENZYME) (AMYL-1,4 TO  
 1,6-TRANSGLUCOSIDASE) (AMYL-1,4-1,6)-TRANSGLUCOSYLASE) (FRAGMENT).  
 DE SBEI OR SBE2-1.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliopsida; eudicotyledons; core eudicot; Rosidae; eurosids II;  
 OC Brassicales; Brassicaceae; Arabidopsids.  
 OC NCBI\_TaxID=3702;  
 RN 111  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA; TISSUE=SEEDLING HYPOCOTYLS;  
 RX MEDIAN=96197401; PubMed=8616246;  
 RA Fisher D.K., Gao M., Kim K.N., Boyer C.D., Gullithan M.J.,  
 RT "Two closely related cDNAs encoding starch branching enzyme from  
 Arabidopsis thaliana."  
 RL Plant Mol. Biol. 30:97-108(1996).  
 CC -1- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF  
 GLYCOGEN.  
 DR EMBL; U18817; AAB0309.1; -;  
 DR Medel; 16400; Atach.Spel;16400.  
 DR InterPro; IPR000461; -;  
 Pfam; PF00128; alpha-amylase; 1.

KW Transferrase; Glycosyltransferase.  
 FT NON\_TER 1  
 SQ SEQUENCE 854 AA; 97229 MW; 6701222ETBD331FC CRC64;  
 Query Match 73.2%; Score 3327; DB 10; Length 354;  
 Best Local Similarity 71.5%; Pred. No. 5,1e-240;  
 Matches 609; Conservative 105; Mismatches 104; Indels 34; Gaps 6;  
 QY 9 IRPPCAPLCSOSTGPHGR---RTSSCSFENKE--AFSRVFGSGSSHESQSSVMVT 63  
 Db 4 VRFPPLPSIKKNSLSHFNEDLRSMNVSFLSRKRSRSGGFAKPPYDSSSLANT 63  
 QY 64 ASKRVLPDGRKEICYSSTQLEAPGVSESVLYTVESLMDKIVDEEVAKESYPMKE 123  
 Db 64 ASER-LRGHSDSSASADQVSDVSDTVSDTVGLAVD-----VQTEEAQETETLDQ 115  
 QY 124 TVSIRKIGS-----KPSIIPPGRGRIYDIPSLTFEPQJLDYRS 165  
 Db 116 TSAISTGSIYKEDPAKMSHVDEVGQRKLPPEDGKRITVDIDMLSHRNLDRYG 175  
 QY 166 QYRLREIDRYEGSDAATSRGYEKFGFSRSETGIYREMAPGATWALIGDPNNMNPNA 225  
 Db 176 QYRLREIDRYEGSDAATSRGYEKFGFSRSETGIYREMAPGATWALIGDPNNMNPNA 235  
 QY 226 DVMTONECGWELFELPNMADGSPPIPHGSRVKIRMDTPSGNDSIPAWIKFSVOAGELP 285  
 Db 236 DVMTONECGWELFELPNMADGSPPIPHGSRVKIRMDTPSGNDSIPAWIKFSVOAGELP 295  
 QY 286 YNGIYDPEEKEKYVFNKNPOPKRKSILRIYESHVSGSTPEYINTFANFRDVLPRIKKL 345  
 Db 296 YNGIYDPEEKEKYVFNKNPOPKRKSILRIYESHVSGSTPEYINTFANFRDVLPRIKKL 355  
 QY 346 GYNAVOMALIOESHYASFGYHTNFYASSRPGTDDLSLIDKHEHIGLVMDIYHS 405  
 Db 356 GYNAVOMALIOESHYASFGYHTNFYASSRPGTDDLSLIDKHEHIGLVMDIYHS 415  
 QY 406 HASNTPLDGLMPDGTGCHPESGRHMMWDRLEKCVSYASHOQALVGDKTIFWIMDK 465  
 Db 416 HASNTPLDGLMPDGTGCHPESGRHMMWDRLEKCVSYASHOQALVGDKTIFWIMDK 475  
 QY 466 FDGFRDGVTSNMYTHHGLQVDFGTNNEYFGATDVAVYVIMLMDMTHGLEPFAVTTI 525  
 Db 476 FDGFRDGVTSNMYTHHGLQVDFGTNNEYFGATDVAVYVIMLMDMTHGLEPFAVTTI 535  
 QY 526 GEDVSGMPTVCIPVEDGSGVEDYRLHMAVADKWEIIOKREDKMGDIYHMLNRRWLE 585  
 Db 536 GEDVSGMPTVCIPVEDGSGVEDYRLHMAVADKWEIIOKREDKMGDIYHMLNRRWLE 595  
 QY 586 KCVSYASHOQALVGDKTIFWIMDKMDYDFAVADKWEIIOKREDKMGDIYHMLNRRWLE 645  
 Db 596 KCVSYASHOQALVGDKTIFWIMDKMDYDFAVADKWEIIOKREDKMGDIYHMLNRRWLE 655  
 QY 646 GEGYLNMGNEFGHPEWIDPREGDLHPSGKFEVPGNNYSYDKCRRRFDIGSKLRYHGM 705  
 Db 656 GEGYLNMGNEFGHPEWIDPREGDLHPSGKFEVPGNNYSYDKCRRRFDIGSKLRYHGM 715  
 QY 706 QERDOALIOHEAVGEMTSEHOYSRDEKDRITVFERGNLYVFENFHTSSYSDRYGCL 765  
 Db 716 QERDOALIOHEAVGEMTSEHOYSRDEKDRITVFERGNLYVFENFHTSSYSDRYGCL 775  
 QY 766 LKRGKRIYDSDNLSLPGGFNRLDSDAEFFTSBGRHDDPCSEMYAIPCRITAVYAAVDD 825  
 Db 776 LKRGKRIYDSDNLSLPGGFNRLDSDAEFFTSBGRHDDPCSEMYAIPCRITAVYAAVDD 835  
 QY 826 EVENE---LEVP 834  
 Db 836 DDDERSLVP 847

RESULT 12  
 Q9SX19 PRELIMINARY; PRT; 841 AA.  
 ID Q9SX19

AC 09SX19:  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
 DE STARCH BRANCHING ENZYME RBE4.  
 GN RBE4.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae;  
 OC Oryza.  
 NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Mizuno K., Tachibana M., Kobayashi E., Kawasaki T., Funane K.,  
 RA Kobayashi M., Baba T.;  
 RT "Molecular cloning and expression analysis of a novel member of starch  
 RT branching enzyme isoform in developing rice seeds";  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB023498; BAA82828.1; -  
 DR InterPro: IPR000461; -  
 DR InterPro: IPR002160; -  
 DR Pfam: PF00128; alpha-amylase; 1.  
 DR ProDom: PD000891; -; 1.  
 DR PRODOM 841 AA; 94779 MW; 9A547A52A6216215 CRC64;  
 SQ SEQUENCE 841 AA; 94779 MW; 9A547A52A6216215 CRC64;

Query Match 72.9%; Score 3315; DB 10; Length 841;  
 Best Local Similarity 74.9%; Pred. No. 3.9e-239;  
 Matches 611; Conservative 66; Mismatches 99; Indels 40; Gaps 6;

36 FNEKFAFSRRVFS-----GK-----SSHEPSSNNMTASKRVLPDGRIEYS 78  
 40 FRKROFSFGVYSCAGAPKVLVPGGSDLLSSAPVEYEQEPEESQIPDDKRVKFE 99  
 79 SSTDLKAGCTV-----EESQVLTDESILMDKIVEDEYKESVPMRETVSIRK 129  
 100 EE-EELPAVAEASIRVVAEDKLESEVIOIE-----ENVTEGVIKADERTVE----- 147  
 130 IGSRSRSTPGRGRIYDIDPSLGFGRHLDYRSQKRLRELDYEGSLDAFSRGYE 189  
 148 --DKRVRIPPDGDKITQIDPMLEGFNHLIDYRSSEKRRRAIDHDEGLDAFSRGYE 205  
 190 KGSRSRSTGTYRREMGATMAALIGDFNNMNPADVMTONEGWEIFLPPNADGSP 249  
 206 KLGFRSAEGITTYREMGAGSALVYGFNNMNPADVMTONEGWEIFLPPNADGSP 265  
 250 IPHGRVATIRMDTPSGNNDSPANIKFSVQAPGELPYNGIYDPEPEEKYVFPKPKRP 309  
 266 IPHGRVATIRMDTPSGVNDSPANIKFPAVOAPGEIPYNGIYDPEPEEKYVFPKPKRP 325  
 310 KSLRTYESHVGMSSTEVINTYANFRDDVLPRIKKLGVNVOALMOHSHYASFGYHYT 369  
 326 NSLRYESHIGMSSPEPKINTYANFRDEVPRIKKLGVNVOALMOHSHYASFGYHYT 385  
 370 NEVYASSRFGPDLKSLIDKAEHLGLVLMIVHSHASTNTLDGLNMFDCGTGHNHSG 429  
 386 NEFAPSSRFEPEDKSLIDKAEHLGLVLMIVHSHASTNTLDGLNMFDCGTGHNHSG 445  
 430 PRGHMMAMDRLTFNYGSEVLEFLLSNARWMLDEYKFDGFRFGVTSMMYTHHGLQVFT 489  
 446 PRGHMMAMDRLTFNYGSEVLEFLLSNARWMLDEYKFDGFRFGVTSMMYTHHGLQVFT 505  
 490 GNRNRYGIVTDAVAVYLMILNDMLHGLEPFAVNTIGEVNPGMPCIPVEGSGVDFR 549  
 506 GNGEYFGFATVDVAVYLMILNDMLHGLEPFAVNTIGEVNPGMPCIPVEGSGVDFR 565  
 550 LHAADVADKWEIIOKREDEMKGDITVHMLTNRRMLECYVIAESHDQALVGDRTAFWLM 609  
 566 LHAADVADKWEIIOKREDEMKGDITVHMLTNRRMLECYVIAESHDQALVGDRTAFWLM 625  
 610 DKMTDFMALDRSTPLIDRGVALHMKIRLITMGAGGEGYLFNFMNGHHPMDIFPRGD 669  
 626 DKMTDFMALDRSTPLIDRGVALHMKIRLITMGAGGEGYLFNFMNGHHPMDIFPRGD 685

OY 670 LHLPSGKFPVGNNTSYDKRRRFDLGNKHLRYHGMQEFQOATOHLEAVGFWTSHOYT 729  
 DB 686 OSLPGSVLPENNNSPDKRRRFDLGNKHLRYHGMQEFQOATOHLEAVGFWTSHOYT 745  
 OY 730 SRKBERDRIIVFERGNLVFVFNHMTSSYSDYRVGCLKPGKRYIVLSDDPLEFGGGRS 789  
 DB 746 SRKHEEKVLIIFERGDVLFVFNHMTSSYSDYRVGCLKPGKRYIVLSDDPLEFGGGRS 805  
 OY 790 HDAEFSEFGVNDRRPFRSMVYTPCRATVAYALVED 825  
 DB 806 HDAEFTADPMDPNRCPSSVSFTPTAVAYALTED 841

RESULT 13  
 ID 024421 PRELIMINARY; PRT; 814 AA.  
 AC 024421:  
 DT 01-JAN-1998 (TReMBLrel. 05, Created)  
 DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)  
 DE STARCH BRANCHING ENZYME IIA (EC 2.4.1.18) (1,4-ALPHA-GLUCAN BRANCHING  
 DE ENZYME) (GLYCOSYL BRANCHING ENZYME) (AMTLO-1,4 TO  
 DE 1,6) TRANSGLUCOSIDASE) (AMTLO-1,4-1,6)-TRANSGLUCOSYLASE) (FRAGMENT).  
 GN SBEI OR SBE2A.  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae;  
 OC Andropogoneae; Zea.  
 NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-97303618; PubMed-9159942;  
 RA Gao M., Fisher D.K., Kim K.N., Shannon J.C., Guiltinan M.J.;  
 RT "Independent genetic control of maize starch-branching enzymes IIA and  
 RT IIB. Isolation and characterization of a Sbe2a cDNA";  
 RL Plant Physiol. 114:69-78(1997).  
 CC -1 CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF  
 CC GLYCOGEN.  
 DR EMBL; U65948; AAB67316.1; -  
 DR Mendel; 26099; Zeamab; Sbe1; 26099.  
 DR InterPro: IPR000461; -  
 DR Pfam: PF00128; alpha-amylase; 1.  
 DR KX Transferase; Glycosyltransferase.  
 FT NON TER  
 SQ SEQUENCE 814 AA; 91865 MW; 0C88B78127511F38 CRC64;

Query Match 71.8%; Score 3261.5; DB 10; Length 814;  
 Best Local Similarity 74.0%; Pred. No. 3.7e-235;  
 Matches 604; Conservative 70; Mismatches 109; Indels 33; Gaps 5;

36 FNEKFAFSRRVFS-----GKSSHEPSSNNMTASKRV-----LPDGRIEYSSST 81  
 7 FRRDARSRYVLSCAGAPKVLVPGGSDLLSSAPVYDQPEELITAEALITYEKKSS 66  
 OY 82 DQLPAPGVSEESQVLTDESILMDKI-----VEDEVNKESVPMRETVSIRKIGS 132  
 DB 67 SPDTTSAVVAEASSGVAEERPELSEVIGVGTTGKIDGAGIKAKAPLVE-----E 118  
 OY 133 KPSRIPPGRGRIYDIDPSLGFGRHLDYRSQKRLRELDYEGSLDAFSRGYKFG 192  
 DB 119 KPRVYIPPDGDKITQIDPMLEGFNHLIDYRSSEKRRRAIDHDEGLDAFSRGYKFG 178  
 OY 193 FSRSEGITTYRREMGATMAALIGDFNNMNPADVMTONEGWEIFLPPNADGSPPIPH 252  
 DB 179 FTSASGKITTYRREMGATMAALIGDFNNMNPADVMTONEGWEIFLPPNADGSPPIPH 238  
 OY 253 GSRVATIRMDTPSGNNDSPANIKFSVQAPGELPYNGIYDPEPEEKYVFPKPKRSL 312  
 DB 239 GSRVATIRMDTPSGVNDSPANIKFPAVOAPGEIPYNGIYDPEPEEKYVFPKPKRSL 298



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QY 313 RYESHVAGNSSTPEVINTYANFPDVLPRIKKLGYNVOLAIOESHYASFGYHVTNFY 372
DB 299 RYESHVAGNSSTPEVINTYANFPDVLPRIKKLGYNVOLAIOESHYASFGYHVTNFY 358
QY 373 AASRRTGPDGLSLDKAHEGLVLMIDVSHASTNLDGLNMDGDTGHHFSGRG 432
DB 359 AASRRTGPDGLSLDKAHEGLVLMIDVSHASTNLDGLNMDGDTGHHFSGRG 418
QY 433 HMMWMDRLNFGSGWEVRLNNAHMLDEYKFGDFRGDGYVSMYTHHGLVDTGNY 492
DB 419 HMMWMDRLNFGSGWEVRLNNAHMLDEYKFGDFRGDGYVSMYTHHGLVDTGNY 478
QY 493 NEYGVANDVAVVYLMIDMIGLEPEAVTIGEDVSGMPTVCIPVEDGVGFDYRLM 552
DB 479 GEYGFANDVAVVYLMIDMIGLEPEAVTIGEDVSGMPTVCIPVEDGVGFDYRLM 538
QY 553 AVAKWVETIIOKRDENKMGDIYHMLNRRMLEKCVSYASHDQALVGDKTAFWLMKD 612
DB 539 AVPKWETIIOKRDENKMGDIYHMLNRRMLEKCVSYASHDQALVGDKTAFWLMKD 598
QY 613 MYDEWALDRPSTPLIDRGVALHKKMRLITMGLGEGYLNFMNGEFGHPWIDPRGDLHL 672
DB 599 MYDEWALDRPSTPLIDRGVALHKKMRLITMGLGEGYLNFMNGEFGHPWIDPRGDLHL 658
QY 673 PGKFPVPCNNYSYDKCRRRFDLGNKSLRYHGMQEPDOAIOHLEAYGEMTSEHOYISRK 732
DB 659 PGKFPVPCNNYSYDKCRRRFDLGNKSLRYHGMQEPDOAIOHLEAYGEMTSEHOYISRK 718
QY 733 DRRDRIYERGNLVEFVNFHMTSSYSDYRVGCLPKGKYKIVLSDPDLFGGRSLSHA 792
DB 719 HEDDKYIIEERDGLVFNFNHMTSSYSDYRVGCLPKGKYKIVLSDPDLFGGRSLSHA 778
QY 793 EHFSEFGWYDNRPSFMYTTPCARTAVYAL--VEDE 826
DB 779 EYFTADMPHNRPCSFYSYAPSRATVAVYAPAGADE 814

RESULT 14
QY 09F0U7 PRELIMINARY: PRT: 823 AA.
ID 09F0U7;
AC 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DE 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
DE STARCH BRANCHING ENZYME 2 (EC 2.4.1.18).
GN SBE2.
OS Triticum aestivum (wheat).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae;
OC Triticum.
OC NCBI_TaxID=4565;
OX
RN
RP
RA SEQUENCE FROM N.A.
RC STEVAIN-CV, CHEYENNE, TISSUE-ENDOSPERM;
RC McCue K.F., Hurman W.J., Tanaka K.K., Anderson O.D.;
RT "Starch Branching Enzymes: Spel and Sbe2 from Wheat (Triticum aestivum
RT cv. Cheyenne): Molecular Characterization, Developmental Expression,
RT and Homolog Assignment by the EMBL/Genbank/DBJ databases.
RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF286319; AAC27623.1;
KW Transferrase; Glycosyltransferase.
SQ SEQUENCE 823 AA; 92970 MW; 58915B0B65A462A CRC64;

Query Match 71.7%; Score 3260.5; DB 10; Length 823;
Best Local Similarity 75.0%; Pred No. 4.5e-235;
Matches 591; Conservative 84; Mismatches 88; Indels 25; Gaps 6;
QY 54 ESDSSNVAVTA---KVLDPGRICEYSSSTDLAAGVSESOVLTVESLIND-- 106
DB 44 KDDSSRAVLSRAAPGKVPDGD-----ESDPLASPAQ--PELQTPEDIEQTAEVNM 95
QY 107 -----DKIVEDEVNK---ESVPMKETSIRK--IGSKPRSPRPGRGQRIYIDIDPSLTF 156

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DB 96 TGGTAKLESSEPTGIVETITDVTKGVKELVGEKRRVVPKRGDGGKITYEID?TLKDF 155
QY 157 ROLHDIRYQYKRLREIDIKYEGSLDAFSGRYEKFGFSRSETGITYRMAAGATVAALIG 216
DB 156 RSHLDIRYSEYRIRRAALDOHGGGLEAFSGRYEKGIFGFSRSETGITYRMAAGATVAALIG 215
QY 217 DFNMMNPNADVMYONCQGWEIFLPNNAGSPAIIPGSGVKIRMDTPSGKNDSPAMIKF 276
DB 216 DFNMMNPNADVMYONCQGWEIFLPNNAGSPAIIPGSGVKIRMDTPSGKNDSPAMIKF 275
QY 277 SVQAPGELPANGITYPPEEEKYVFKNPOPKRKSRLRYESHVAGNSSTPEVINTYANRD 336
DB 276 SVQAPGELPANGITYPPEEEKYVFKNPOPKRKSRLRYESHVAGNSSTPEVINTYANRD 335
QY 337 DVLPRIKKLGYNVOLAIOESHYASFGYHVTNFPAASRFGTDDKSLDKAHEGL 396
DB 336 EYLPRIKRLGYNVOLAIOESHYASFGYHVTNFPAASRFGTDDKSLDKAHEGL 395
QY 397 LVLMIDVSHASTNLDGLNMFDTGHHFSGRGHMMWMDRLNFGSGWEVRLN 456
DB 396 LVLMIDVSHASTNLDGLNMFDTGHHFSGRGHMMWMDRLNFGSGWEVRLN 455
QY 457 ARWMLDEKFPDFGFDVTSMTYTHHGLVDTGNTNEYFGVATDYAVYIYLMIDMTH 516
DB 456 ARWMLDEKFPDFGFDVTSMTYTHHGLVDTGNTNEYFGVATDYAVYIYLMIDMTH 515
QY 517 GLFPAVAVTIGEDVSGMPTVCIPVEDGVGFDYRLMAVADKVEIIOKRDENKMGDIYH 576
DB 516 GLFPAVAVTIGEDVSGMPTVCIPVEDGVGFDYRLMAVADKVEIIOKRDENKMGDIYH 575
QY 577 MLTNRRMLEKCVSYASHDQALVGDKTAFWLMKDMDYDPMALDRPSTPLIDRGVALHKKM 636
DB 576 MLTNRRMLEKCVSYASHDQALVGDKTAFWLMKDMDYDPMALDRPSTPLIDRGVALHKKM 635
QY 637 ILLITMGLGEGYLNFMNGEFGHPWIDPRGDLHPSKFPVPCNNYSYDKCRRRFDLGN 696
DB 636 ILLITMGLGEGYLNFMNGEFGHPWIDPRGDLHPSKFPVPCNNYSYDKCRRRFDLGN 695
QY 697 SKRLRYHGMQEPDOAIOHLEAYGEMTSEHOYISRKDRDRIYERGNLVEFVNFHMTSS 756
DB 696 ADPLRYHGMQEPDOAIOHLEAYGEMTSEHOYISRKDEKVIILFEFGDLVFNFNHMTSS 755
QY 757 SYSDYRVGCLPKGKYKIVLSDPDLFGGRSLSHAHEFSEFGWYDNRPSFMYTTPCART 816
DB 756 SYSDYRVGCLPKGKYKIVLSDPDLFGGRSLSHAHEFSEFGWYDNRPSFMYTTPCART 815
QY 817 AVYVALVE 824
DB 816 AVYVALVE 823

RESULT 15
ID P93691 PRELIMINARY: PRT: 823 AA.
AC P93691;
DT 01-MAY-1997 (TEMBLrel. 03, Created)
DT 01-MAY-1997 (TEMBLrel. 03, Last sequence update)
DT 01-MAY-2001 (TEMBLrel. 16, Last annotation update)
DE 1,4-ALPHA-GLUCAN BRANCHING ENZYME II PRECURSOR (EC 2.4.1.18) (GLYCOGEN
DE BRANCHING ENZYME) (ANYLO- (1,4 TO 1,6) TRANSGLUCOSIDASE) (ANYLO- (1,4-
DE 1,6)-TRANSGLUCOSYLASE).
GN SBE1 OR SBE2.
OS Triticum aestivum (wheat).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae;
OC Triticum.
OC NCBI_TaxID=4565;
OX
RN
RP
RA SEQUENCE FROM N.A.
RC STEVAIN-CV, FIELDER;
RC Nair R.B., Baga M., Scoles G.J., Kartha K.K., Chibbar R.N.;
RL Plant Sci. 0:0-0(0).

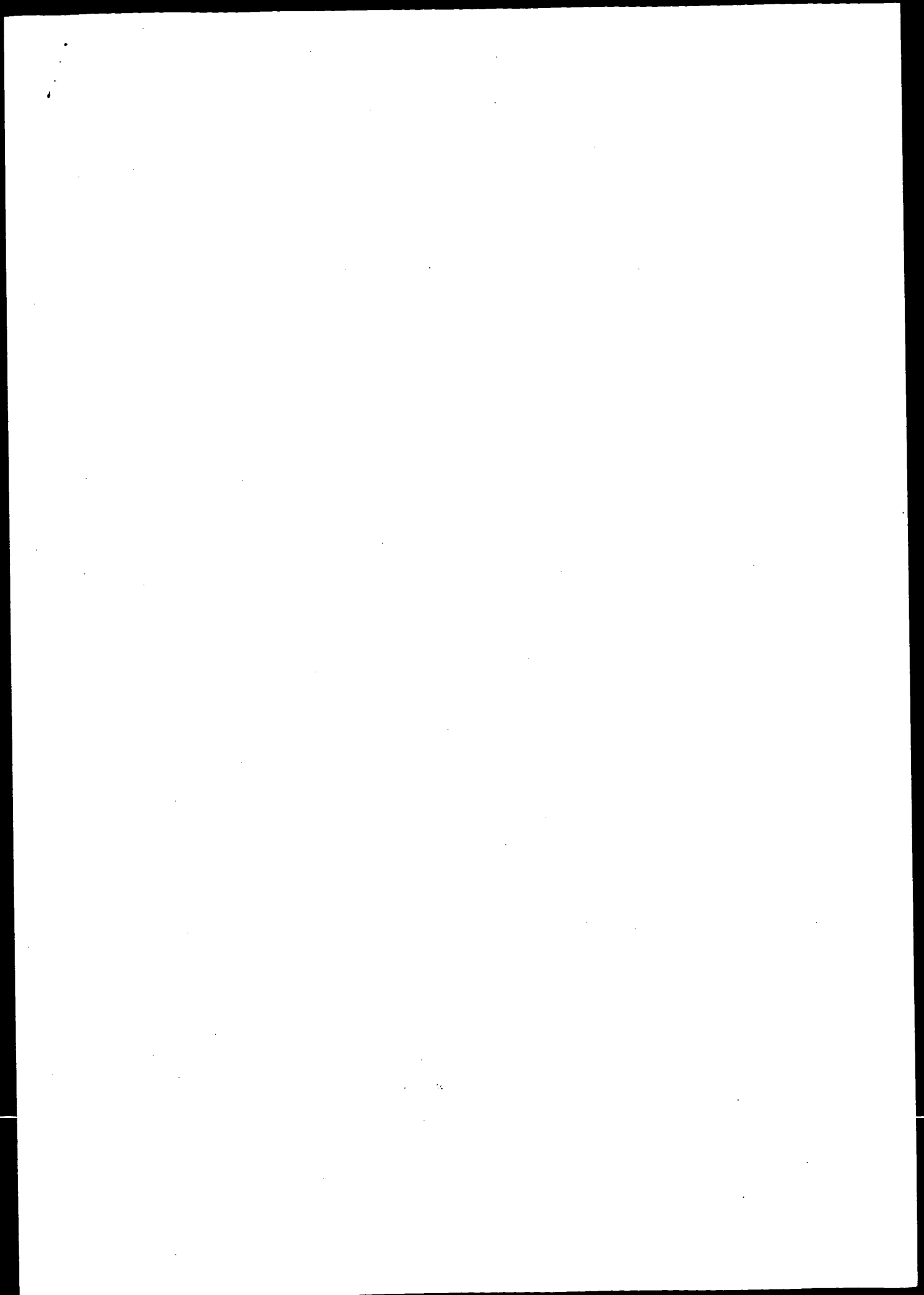
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Job time: 146 sec

9

QY	54	ESSSSNNVMTAS----	KRVLPDGRLEC	SSSSDLOE	AGTYS	SESSOVL	TDES	LMD---	106
		: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	
Db	44	KRSSAAVYS	SRASPEK	YLPVGD-----	ESDDLAS	PAO--	PEELIO	PEIEE	TEA
		: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	95
QY	107	----	DRIVEDEYNK----	ESVPMRE	TVSIRK--	-IGSKRST	IPRPGRO	RIATY	IDDP
		: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	156
Db	96	TGGTAKLES	SEP	TGQIV	ET	LINDG	TVTK	YK	VELV
		: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	155
QY	157	ROHLD	YR	YOQYR	KRLBE	IDK	YGS	SLDA	F
		: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	216
Db	156	RSHLD	YR	SEYER	IRAI	AD	IOH	EG	GLEA
		: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	215
QY	217	DFNNM	P	NAD	VT	ONE	CG	W	ET
		: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	276
Db	216	DFNNM	P	NAD	VT	ONE	CG	W	ET
		: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	275
QY	277	SWOAP	EL	P	Y	NG	I	Y	D
		: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	336
Db	276	SWOAP	EL	P	Y	NG	I	Y	D
		: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	335
QY	337	DVL	P	R	K	I	G	Y	A
		: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	396
Db	336	EVL	P	R	K	I	G	Y	A
		: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	395
QY	397	LVLMD	I	V	H	S	H	A	S
		: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	456
Db	396	LVLMD	I	V	H	S	H	A	S
		: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	455
QY	457	AAW	M	I	D	E	T	E	K
		: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	516
Db	456	AAW	M	I	D	E	T	E	K
		: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	515
QY	517	GLEP	P	A	V	I	T	E	G
		: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	576
Db	516	GLEP	P	A	V	I	T	E	G
		: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	575
QY	577	M	T	N	R	M	L	E	K
		: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	636
Db	576	M	T	N	R	M	L	E	K
		: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	635
QY	637	I	R	L	T	M	G	I	G
		: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	696
Db	636	I	R	L	T	M	G	I	G
		: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	695
QY	697	S	K	H	I	R	T	M	G
		: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	756
Db	696	S	K	H	I	R	T	M	G
		: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	755
QY	757	S	Y	S	D	R	V	G	C
		: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	816
Db	756	S	Y	S	D	R	V	G	C
		: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	815
QY	817	A	V	Y	A	I	A	L	E
		: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	
Db	816	A	V	Y	A	I	A	L	E
		: : : : : :	: : : : : :	: : : : : :	: : : : : :				



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 7, 2001, 11:13:33 ; Search time 25.03 Seconds

(without alignments)  
2024.836 Million cell updates/sec

Title: US-09-297-703a-29

Perfect score: 4545  
Sequence: 1 MGHYISGIRPCAPLCKSQ.....AVVYALVEDEVENLEFPVAG 836

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A.GeneSeq-0601:\*

- 1: /SIDSB8/gcgdata/geneSeq/AA1980.DAT:\*
- 2: /SIDSB8/gcgdata/geneSeq/AA1981.DAT:\*
- 3: /SIDSB8/gcgdata/geneSeq/AA1982.DAT:\*
- 4: /SIDSB8/gcgdata/geneSeq/AA1983.DAT:\*
- 5: /SIDSB8/gcgdata/geneSeq/AA1984.DAT:\*
- 6: /SIDSB8/gcgdata/geneSeq/AA1985.DAT:\*
- 7: /SIDSB8/gcgdata/geneSeq/AA1986.DAT:\*
- 8: /SIDSB8/gcgdata/geneSeq/AA1987.DAT:\*
- 9: /SIDSB8/gcgdata/geneSeq/AA1988.DAT:\*
- 10: /SIDSB8/gcgdata/geneSeq/AA1989.DAT:\*
- 11: /SIDSB8/gcgdata/geneSeq/AA1990.DAT:\*
- 12: /SIDSB8/gcgdata/geneSeq/AA1991.DAT:\*
- 13: /SIDSB8/gcgdata/geneSeq/AA1992.DAT:\*
- 14: /SIDSB8/gcgdata/geneSeq/AA1993.DAT:\*
- 15: /SIDSB8/gcgdata/geneSeq/AA1994.DAT:\*
- 16: /SIDSB8/gcgdata/geneSeq/AA1995.DAT:\*
- 17: /SIDSB8/gcgdata/geneSeq/AA1996.DAT:\*
- 18: /SIDSB8/gcgdata/geneSeq/AA1997.DAT:\*
- 19: /SIDSB8/gcgdata/geneSeq/AA1998.DAT:\*
- 20: /SIDSB8/gcgdata/geneSeq/AA1999.DAT:\*
- 21: /SIDSB8/gcgdata/geneSeq/AA2000.DAT:\*
- 22: /SIDSB8/gcgdata/geneSeq/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4545	100.0	836	19	AAW62599
2	3949	86.9	848	19	AAW62600
3	3405.5	74.9	878	18	AAW19113
4	3373	74.2	858	21	AAW39092
5	3356	73.8	882	17	AAW63399
6	3335	73.4	847	17	AAW64000
7	3315	72.9	841	19	AAW41763
8	3309.5	72.8	842	17	AAW3804
9	3241.5	71.3	768	20	AAW6917
10	3219.5	70.8	721	21	AAW39093
11	3180	70.0	825	15	AAW60811

12	3169	69.7	871	19	AAW70895
13	3160	69.5	799	19	AAW6489
14	3159	69.5	799	18	AAW19212
15	3140.5	69.1	693	21	AAW39094
16	2745	60.4	592	21	AAW84410
17	2745	60.4	758	21	AAW84408
18	2710.5	59.6	888	21	AAW84416
19	2377.5	52.3	481	19	AAW62650
20	2192.5	48.2	906	19	AAW71290
21	2192.5	48.2	906	19	AAW69300
22	2130.5	46.9	820	15	AAW53228
23	2124	46.7	751	13	AAW35862
24	2124	46.7	759	13	AAW70896
25	2124	46.7	822	19	AAW56490
26	2124	46.7	844	18	AAW19213
27	2121.5	46.7	820	15	AAW47468
28	2117.5	46.6	833	21	AAW32466
29	2107	46.4	807	20	AAW06916
30	2016	44.4	686	21	AAW49603
31	1597.5	35.1	368	21	AAW15423
32	1592.5	35.0	367	21	AAW15424
33	1426.5	31.4	336	21	AAW15425
34	1242	27.3	228	19	AAW62649
35	940	20.7	212	21	AAW84411
36	927	20.4	212	21	AAW84409
37	576	12.7	762	21	AAW90977
38	572	12.6	639	12	AAW11271
39	571.5	12.6	630	22	AAW69074
40	571.5	12.6	785	19	AAW70886
41	570	12.5	621	21	AAW19285
42	550.5	12.1	731	22	AAW79423
43	542.5	11.9	652	16	AAW80037
44	542.5	11.9	652	17	AAW96109
45	541.5	11.9	753	20	AAW37247

#### ALIGNMENTS

RESULT	1	ALIGNMENTS
AAW62599	Standard; Protein; 836 AA.	
XX	AAW62599;	
AC	21-SEP-1998 (first entry)	
DT	Cassava starch branching enzyme II (SBE II).	
XX	Starch branching enzyme; SBE; cassava.	
XX	Manihot esculenta.	
XX	WO9820145-A2.	
PN	14-MAY-1998.	
XX		
XX	04-NOV-1997; 97WO-GB03032.	
PF	05-NOV-1996; 96GB-0023095.	
XX		
PA	(NAT) NAT STARCH & CHEM INVESTMENT HOLDING COR.	
XX	Jobling SA, Safford R;	
PI	WPI; 1998-286958/25.	
XX	N-PSDB; AAV38719.	
DR	Starch branching gene from cassava - useful for producing altered	
XX	plants giving modified starch	
PT	Claim 1; Fig 4; 67pp; English.	
PS		
XX		

Maize branching en  
Zea mays starch br  
Corn starch branch  
Arabidopsis thalia  
Amino acid sequenc  
Amino acid sequenc  
Consensus sequence  
Starch branching e  
Potato starch bran  
Potato class B sta  
Rice starch branch  
Branching enzyme.  
Maize branching en  
Zea mays starch br  
Corn starch branch  
Branching enzyme o  
Maize starch bran  
wSBE I-Da amino ac  
Glycogen branching  
Arabidopsis thalia  
Arabidopsis thalia  
Starch branching e  
Amino acid sequenc  
Amino acid sequenc  
N. denitrificans a  
B. stearothermophil  
A. aquiflex aeolicus V  
Protein encoded by  
A polypeptide with  
Corynebacterium gl  
Bacillus stearothe  
Starch-branching-e  
Protein involved 1



```

QY 356 QEHSTYASTGHTNTNFAASRRFGTPDDLSKIDKAHELGVLMDIVHSHASTITDGL 415
D 361 qehsyasfgyhtntnfapsrrfgtpddlskldkahelgvlvmdivshasmtldgl 420
QY 416 NMFEDGTGHTFSGPGHHMMDSRLFNFGSGEVRFLLSNARKWLDEYKDFGFRPGVT 475
D 421 nmfdgtdshtfsgprghmmwdsrlfnfgsgewrlflsnarwleeyrtdgfrfdgvt 480
QY 476 SMATTHGLQVDFGTGNYNMEFGYATDVAVVYLMINDMIGLPEAVTIGEDVSGMPTV 535
D 481 smmytphglqvafgtgnyeyfgyatdvavlylmvndmimglfpavtligedvsgmptv 540
QY 536 CIPVEDGAGVGPYRLHMAVADKWEIIOKRBDMKMDIVMLTNRRLKCYASASHD 595
D 541 cipvedgagvgtdyrlhmadkweilkkridewkmqdivhltlnrrwlckvayashd 600
QY 596 QALVGDKTIAFWLMDKMDYDFMALDRPSTPLIDRGVALHKKIRLITMGIGEGEYLNMG 655
D 601 qalvgdktiafwlmdkmdydfmaldrpstplidrgvalhkkirlltmglgsegylntmgn 660
QY 656 EFGHEWIDFPRGDLHPSGKFPVGNNSYDKCRREFDLGNSKRLRYHGMQEFDAIOHL 715
D 661 efghewidfprgdhlpsgkfvpgnnsydkcrrrefdlgdadylyhgmqefdaqmhl 720
QY 716 EEA YGFMTEHQYISRKDERDRIIVPERGNLYFVFNHMTSSSDYRVGCLAKGKTKIVL 775
D 721 eea ygmtehqyisrkdegrlrvpergnlyfvfnhmtsssdryvgclakgktyivl 780
QY 776 DSDPLFEGFRLSHDAEHSFEGMYDNRRSPFVYPTCTAVVYALVED-----EVE 828
D 781 dsdplfegfgrlshdaehsfegmydnrrspfvypctavvyalved-----eve 840
QY 829 NELEPVAG 836
D 841 nelevpag 848

```

RESULT 3  
AAW19113  
ID AAW19113 standard; Protein; 878 AA.  
XX  
AC AAW19113;  
XX  
D 26-AUG-1997 (first entry)  
XX  
DE Potato starch branching enzyme II.  
XX  
KW Starch branching enzyme II; beii gene; potato; transgenic plant;  
KW amylopectin; amylose; starch.  
XX  
OS Solanum tuberosum.  
XX  
FH Key Location/Qualifiers  
FH Peptide 1.48  
FH Protein 49..878  
FH Misc-difference 33  
FH /note= "residue 33 was not detd. owing to  
FT degeneracy of coding sequence (codon NTT)"  
FT Misc-difference 406  
FT /note= "residue 406 was not detd. owing to  
FT degeneracy of coding sequence (codon TTN)"  
FT Misc-difference 570  
FT /note= "residue 570 was not detd. owing to  
FT degeneracy of coding sequence (codon TNY)"  
XX  
PN MO9720040-A1.  
XX  
PD 05-JUN-1997.  
XX  
PF 28-NOV-1996; 96WO-SE01558.

```

XX 19-APR-1996; 96SE-0001506.
PR 29-NOV-1995; 95SE-0004272.
XX
PA (EKBB/) EK B.
PA (KHOS/) KHOSNOODI J.
PA (LARS/) LARSSON C.
PA (LARS/) LARSSON H.
PA (RASK/) RASK L.
PA (AMTL-) AMTLOGENE HB.
XX
PI Ek B, Khosnoodi J, Larsson C, Larsson H, Rask L;
DR WPI: 1997-310596/28.
XX N-PSDB; AAT69587.
XX
PT Isolated potato starch branching enzyme II - useful for altering
PT degree of amylopectin branching and amylopectin/amylose ratio in
XX potato starch
XX
PS Claim 1; Page 12-15; 24pp; English.
XX
CC The amino acid sequence (AAW19113) for potato starch branching enzyme
CC II (BEII) was deduced from a cDNA clone (AAT69587) isolated from
CC tuber cDNA using primers (AAT69588-89) based on BEII tryptic
CC peptides. It shows 68% identity to potato starch branching enzyme
CC I and about 80% identity to BEII from other plant species. BEII,
CC or functional active parts of the enzyme, can be expressed in
CC transgenic potatoes. The starch obt. from such plants will show a
CC changed pattern of amylopectin branching and an altered amylopectin
CC to amylose ratio.
XX
SQ Sequence 878 AA;

```

Query Match 74.9%; Score 3405.5; DB 18; Length 878;  
Best Local Similarity 72.2%; Pred. No. 0;  
Matches 624; Conservative 91; Mismatches 114; Indels 35; Gaps 5;

```

QY 4 YTTGISRPPCAP-LCKSQSTGFHGYRTSSCLSFNFKKFAFRVYSGKSHSDSSNNVY 62
D 3 ytlsgyrtfrcvpsvyksngfssngdrtmanxvflkkslrlaekssyssearptv 62
QY 63 TASKRVL-PDGRIEYSSSTIDQLEAPGVSESOYLTDESLIMD---KIVEEV--- 114
D 63 aasgkvlvptgtdsssssdgfeftetpennspastdssstmeaagtkendavps 122
QY 115 -----NKESVPMREYISIRKIGS-----KPSITPPGRGQRTYD 148
D 123 sdltgsveeldfssslqldgeygleeskltntseetlidesdrtireglppgjqklye 182
QY 149 IDPSLTGFROHLDYRSQYKRLREEDIKYEGSLDAFSRGYKFGFSRSGTGYREAPG 208
D 183 idp slt gfr oh ldy r sqy krl r e e d i k y e g s l d a f s r g y k f g f s r s g t g y r e a p g 242
QY 209 ATMAALIGDPNNKMPADYMTONEGCGWEIFLPNNADSPPIPHGSRVAKIRMDPPSGNKD 268
D 243 aqsaalligdfinwdanadmtnefgyweilfipnvdspipbgsrvtklmdtprsyvk 302
QY 269 SIPAWIKFSVOAGELPYNGIYDPPREEKYVFKNPQKRKSLRITYSHGMSSTEPVI 328
D 303 sipawinyslqldpelpyngilydppreeerylfghprkpkkslryeshgmspepk 362
QY 329 NTYANFRDDVLRIRKLGYNALVMAIOEHSYASFGYHVNFFAASRFGTDPDLKSLI 388
D 363 ntyanfrddv l r i r k l g y n a l v m a i o e h s y a s f g y h v n f f a a s r f g t d p d l k s l i 422
QY 389 DKAHELGLIYMDIVHSHASTITDGLMFPDGTGHTFHSGRGHMMWMDSRLFNFGSWE 448
D 423 dkaheglivvmdivshasmtldglmftdgtdshtfhsgrgyhmmwdsrlfnfgswe 482
QY 449 VLRFLLSNARKWLDEYKDFGFRPGVTSMATTHGLQVDFGTGNYNMEFGYATDVAVVYL 508
D 482 vlrflflsnarwleeykdfgfrpgvtsmatthglqvdfgtgnyneefgyatdvavvy 508

```

Db 483 vlyllsnaarwldelfdfrfdgvtsmmythhjsvfgftgnyeeeyfglatdadvayyl 542  
QY 509 MLNDMTHGLEPEAVTIGEDVSGMPYVCIPVEEGCGYGFDRHMANVADKWVELIQRDEED 568  
Db 543 mlvndllhghlfpdaitlgedvsgmptltxlrvqdgvgvldfrrlmaladkwvlelkrtdd 602  
QY 569 WKMDIVHMLTNRRLKCVSYAESHDQALVGDKTIAFWIMDKDMYDFMALDRPSPLID 628  
Db 603 wrvqglvhltnrrtwsekwasyaeshdaqlygdktiafwimdkdmvdfmaldrpsstltd 662  
QY 629 RGVALLHKIRLITITGLGEGEYLNPMGNEFGHPWIDFPRGDLHLPGCKFVPGNNYSYDKC 688  
Db 663 rgialhkhmlrlvtnglsggeylnfmgnefghpewidfpnaeqhlsdsvlpgnqfsgdkc 722  
QY 689 RRRPDLGSKHLRYHGMQEPDQAIQHEAVGFWTSEHOYISRKEDRRIIVERGNLVEF 748  
Db 723 rrrldgdaeyllyrglgeiframyldckyeftntsehgffsrkdegdrmlvfekgnlvf 782  
QY 749 VNFHWTSISDYRGCLKPKGKYKIVLSDDPLEFGFGRLSHDAEHFSPGQWYDNRPSPF 808  
Db 783 vlnfhwtsysdyrgclpkpkykvalsdppltfgyfgrldhnaeyftfegwyddrpsrl 842  
QY 809 WYTPCRAVAVYALVEDEVENLE 832  
Db 843 mvyapstlavayalvdkeeeeee 866  
RESULT 4  
ID AAC39092 standard; Protein: 858 AA.  
AAC39092;  
AC AAC39092;  
XX 18-OCT-2000 (first entry)  
DT XX  
XX Arabidopsis thaliana protein fragment SEQ ID NO: 48321.  
DE XX  
XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX Arabidopsis thaliana.  
OS XX  
XX EPI033405-A2.  
PN XX  
XX 06-SEP-2000.  
PD XX  
XX 25-FEB-2000; 2000EP-0301439.  
PF XX  
XX 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 23-APR-1999; 99US-0130891.  
PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 07-MAY-1999; 99US-0132487.  
PR 11-MAY-1999; 99US-0132863.  
PR 14-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134270.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139452.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139839.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 02-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 19-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.



Db 835 aavddddderslvp1 851

# RESULT 5

AAW06399 standard; Protein; 882 AA.

AAW06399;

25-FEB-1997 (first entry)

Class A starch branching enzyme (19con.seq).

Starch branching enzyme; SBE; class A; class B; Solanum tuberosum; amylose; viscosity; potato.

Solanum tuberosum.

Key Location/Qualifiers  
Peptide 1..49  
FT /label= sig\_peptide  
FT 50..882  
FT Protein /label= mat\_protein

MO9634968-A2.

07-NOV-1996.

03-MAY-1996; 96WO-GB01075.

10-APR-1996; 96GB-0007409.

05-MAY-1995; 95GB-0009229.

(NAT) NAT STARCH & CHEM INVESTMENT HOLDING COR.

Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;  
Sidebottom CM, Westcott RJ;

WPI: 1996-506170/50.  
N-PSDB; AAT42630.

New potato plant starch having high amylose content - also class A starch branching enzyme and corresp. DNA to alter the viscosity of starch; for use in food, biodegradable products, adhesives, etc.  
Claim 39-40; Page 42-46; 142pp; English.

Class A starch branching enzyme (SBE) has been obtained from potatoes. In class A SBE moles, a flexible N-terminal domain, is found, which is not found in class B moles.

Sequence 882 AA;

Query Match 73.88; Score 3356; DB: 17; Length 882;

Best Local Similarity 70.98; Pred. No. 7.5e-300; Mismatches 119; Indels 38; Gaps 6;

Matches 617; Conservative 96; Mismatches 119; Indels 38; Gaps 6;

4 YTIGIRPCAP-LCKSOSTGFGHYRTTSCLSFNFKAFSRVFSKSSSHSDSSVMV 62

3 YLISGVIFPVPSYKSGFNGSDGRNANVSFLKHSIRKLAESYNSFIRPSTV 62

63 TARKRVLPDGRICYSSTQDLAPGTVSESOVLTVESLIMDD---KIVEDEV--- 114

63 aasgkvlvpgsgssssstqdfteletspenastdvsstmehasqklteendvps 122

115 -----NKSVMRETVSIRKTS-----KPSIPPGRCORIVD 148

123 sdtgsveelafasidqgeggkleeekltintseetlidesdrtiregipppgqklye 182

149 IDPSLTGRHLDYRYSQYKRLREIDIKYEGSLDAFSGYKRFSGSSENGITREWAPG 208

183 idpilttyghldyrysgykkrlrealdkyeggleafstrgyekmgftrsaqgilyrewaig 242

QY 209 ATWALIGDFRNNMPNADVTQONCEGVMEFLFPNNADGSPPIPHGSVKIRMDT PEGNKD 268

Db 243 aqsallgdtrnnwddandimlinefywelflpnnvdgsparlphgervklrmdtpgvd 302

QY 269 SIPAWIKFSVQAGEELPYNGIYDPPEEEKYVFRNPKRPSLRIRYESHVGM:STEPVY 328

Db 303 sipawlnyslqldpdlpynglhydppeeeeylignpypkpkstlryeshlmg:spexk 362

QY 329 NTYANFRDVLPRIKKLGYNALQIQAESHYASFGYHTNTNYYAASSRCRTPUDLSLT 388

Db 363 nsyvnfidevlprikkgynalqimaqemssyyslgyhvnltfapsrtfcpudlksll 422

QY 389 DKAEHLGLVIMDIVSHASTNTLDGLNMEGDGDTGHTFHSGRFGHMMMSRLVNGSWE 448

Db 423 dkahelgivvlimdivshasnntldglmifctldscyfhsgatgyhmmwsrlhnygnwe 482

QY 449 VLREFLSNARWMLDEYKFGDFRFDGVTSMYTHGLQVDFGTNEXFGYATDIDAVYVL 508

Db 483 vlyrlsnarwmldefkfgdfrrfdgvtssmyihnglsvfgtgyeeyfglatdvdavyl 542

QY 509 MLNDMIRGLPEEAVTIGEDVSGMPVCIPEVDGSGVFEDRLAHAAVADKWEI:OKRDED 568

Db 543 mlvndlhglfpdaltlgedvsgmpfcipvqegvgfydzlhmaladk:tel.krded 602

QY 569 WKMGDIVHMLNRRMLKCVSYASHDQALVGDRTIAFWLMDKMDYPMALDRPSTPLID 628

Db 603 wmgdivhmlnrrmlkcvsyashdqlvgdrtiafwlmdkmdyfmaldrxpsta:ld 662

QY 629 RGVALHKKMIRLITMGLGEGYLNFMGNFEGHPWIDPRDGLH:PSGKFVGNYSYDKC 688

Db 663 rgalhkkmrlitmglggeylnfmgnefghpewidpraeqhlvsdgsavlpgn:fsydkc 722

QY 689 RRRPDLGSKHRRHGMQEPDQALQHEAAGCFMTESEHGYTSRDEDRITVE:RGNLVE 748

Db 723 rrrldgdaeylrrygldeidpmlylekyemfsehgflstrdegdmv:fakgnlvf 782

QY 749 VNFHWTSSYSDYRVGLCPGKRYKIVLDSDDPLRGGFRRLSHDSEHSGEYWNRPBSF 808

Db 783 vnfhwtsysdyrvlclpkpgykvaldsddpllrgyigrldhnaeyl:legwydprst 842

QY 809 MYTTCRTAVYVALV---EDEVENLEPVA 835

Db 843 myapoktaavyalvdkeeeeeevea 872

RESULT 6  
AAW06400 standard; Protein; 847 AA.

AAW06400;

25-FEB-1997 (first entry)

Class A starch branching enzyme (psbe2con.seq - clone psj90).

Starch branching enzyme; SBE; class A; class B; Solanum tuberosum; amylose; viscosity; potato.

Solanum tuberosum.

Key Location/Qualifiers  
Peptide 1..11  
FT /label= sig\_peptide  
FT 12..847  
FT Protein /label= mat\_protein

WO9634968-A2.

07-NOV-1996.

03-MAY-1996; 96WO-GB01075.



PR 10-APR-1996: 96GB-0007409.  
 PR 05-MAY-1995: 95GB-0009229.  
 PA (NATT) NAT STARCH & CHEM INVESTMENT HOLDING COR.  
 PI Cooke D, Debel M, Gidley MJ, Jobling SA, Safford R;  
 PI Sidebottom CM, Westcott RJ;  
 XX WPI: 1996-506170/50.  
 DR N-PSDB; AAT42631.  
 XX  
 XX New potato plant starch having high amylose content - also class A  
 PT starch branching enzyme and corresp. DNA to alter the viscosity of  
 PT starch; for use in food, biodegradable products, adhesives, etc.  
 XX  
 PS Disclosure: Fig 12; 142pp; English.  
 CC  
 CC Class A starch branching enzyme (SBE) has been obtained from  
 CC potatoes. In class A SBE mols., a flexible N-terminal domain,  
 CC is found, which is not found in class B mols.  
 XX  
 SO Sequence 847 AA:

Query Match 73.4%; Score 3335; DB 17; Length 847;  
 Best Local Similarity 73.6%; Pred. No. 6e-298;  
 Matches 608; Conservative 84; Mismatches 98; Indels 36; Gaps 5;

QY 46 VESGKSHSDSSNMVYASKRVL-PDGRICYSSTDLAPQVSESOVLTVESLI 104  
 DB 12 llaeksynsefrstvaeasgkvlvypgtqsdssstscqfctcspenspaatvdast 71  
 QY 105 MDD-----KIVDEV-----NRESVPMRETVSIRKIGS----- 132  
 DB 72 mehasqiktendvpsadltgsveeldfasslqlegqkleestklntseetlidesdt 131  
 QY 133 -KPSRIPPGSGRIYIDISLGFROHLDYRSQYKRLKEEDIKTSGIDAFSGYERF 191  
 DB 132 lregrlpppglqgklyedplltlntgqldyrsyqkltreaidkyeggleatsrgyekm 191  
 QY 192 GFSRSETGITYREMAPGATWAALIGDFNMNPNADVYTONCEGWEIFLPNNADSGPPRP 251  
 DB 192 gftsatgilyrewapagaaligdmndandlmtnefgvweilfpnnvdgsalp 251  
 QY 252 HGSRVKTIRMOTPGSGNKRISIPAWIKFSYQAPGELPYNGIYYDPPEEKYVKNPQRPKPS 311  
 DB 252 hgstvklrmtlpsqvkdsipawinsyqjpdelpyngiyydppeeryfqprrpkpks 311  
 QY 312 LRITYSHVNGSTEPVINTYANFRDVLPRIKKLGVNAVQALAIQHSYTSFQHYVTF 371  
 DB 312 lrlyeshlmgaspeprklnsyntfdevlprlkllynaavqlmaigehsyasfgyhvnf 371  
 QY 372 YAASSRRTGTDLKLIDRAHELGILLVMDIYVSHASTNTLDGLNFDOTDHYHSGPR 431  
 DB 372 fapsstfipddklslidkabelgylvndlvshasnmtdlglimfdgldscyhsgr 431  
 QY 432 GHMMMDSLRFNNGSWEVLRFLISNARWMLDXYKDFGFFDGVTSMTYTHGLQVDFGN 491  
 DB 432 gylmmmdslrlfngnwevlyllsnarwmldefkldgtrfdgtvtsmtythnglsvgffgn 491  
 QY 492 YNEFYATDVAVYVIMLNDMIGLFPPEAVTIGEDVSGMPVTCIPYEDGCGEFDRLH 551  
 DB 492 ynefyatdvavylimlndmiglfppeavtigedvsgmpvtcipydgdgfdyrlh 551  
 QY 552 MAVADKVVITIKRQEDMKMDIYHMLTNRNMLEKCVASASHOALVGDITAFWMLMDK 611  
 DB 552 maladkvwitlkrqedmkmdiyhmltnrnmllekcvasashoalvgditiawmlmdk 611  
 QY 612 DMVDFMALDRPSTPLIDGVALHKMIRLITMGIGEGSLTNWGEFGEHPEKIDFPRGDLH 671  
 DB 612 dmvdftmaldrpstplidgvalhkmirlitmgigegsltnwgefgehpekidfprgdh 671  
 QY 672 LPGSKFVPGNNNSYDKCRRRRDLGNSKHLRYHGQEFQDAIQHLEAVYGFWTSHQYISR 731

DB 672 lsdasvlpnqnsydkcrrrrfdlgdaeylryrlgqefdramyldckyefntseqlfist 731  
 QY 732 KDERDLIYFERGNLYEVNFNHTSYSDYRGYCAKPKKRYKVLDSDDLPGGGRSLSD 791  
 DB 732 kdegdrmiyfergnlyevnfhnhtsydyrgyckpkkykvaldsddlpgggrslsd 791  
 QY 792 AEHFSFEGWYDNKRPSFEMVYTPCORTAVVYALV--BDEVENELEPYA 835  
 DB 792 aeyftfegwyddprslmyaportavvayalvdkeeeeeevea 837

## RESULT 7

AAW41763  
 ID AAW41763 standard; Protein; 841 AA.  
 XX  
 XX AAW41763;  
 AC AAW41763;  
 XX  
 XX  
 DT 01-MAY-1998 (first entry)  
 XX

DE Rice type IV starch branching enzyme.  
 XX

KW Rice; type IV starch branching enzyme; amylopectin synthesis.  
 XX

OS Oryza sativa.  
 XX

PN JP10004970-A.  
 XX

PD 13-JAN-1998.  
 XX

PF 24-JUN-1996; 96JP-0162983.  
 XX

PR 24-JUN-1996; 96JP-0162983.  
 XX

PA (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENYUSHO.  
 PA (MITK) MITSUI TOATSU CHEN INC.  
 DR WPI: 1998-133625/13.  
 DR N-PSDB; AAV05639.  
 XX

PT Rice starch branching enzyme gene - synthesises amylopectin to yield  
 PT high quality starch  
 PS

PS Claim 1; Pages 5-8; 13pp; Japanese.  
 XX

CC The present sequence is the rice type IV starch branching  
 CC enzyme, which has the ability to synthesise amylopectin. The  
 CC quality of starch is improved by the use of the protein.  
 XX

SO Sequence 841 AA;

Query Match 72.9%; Score 3315; DB 19; Length 841;  
 Best Local Similarity 74.9%; Pred. No. 4.1e-296;  
 Matches 611; Conservative 66; Mismatches 99; Indels 40; Gaps 6;

QY 36 FNFKEAFSRRVTS-----GK-----SSHSDSSNMVYASKRVLPDGRICYS 78  
 DB 40 firkdsfrfgvscagapgvkvlvpggsddlssaeqvetqeqeegpddkkyvpe 99  
 QY 79 SSTDLAPAGTYS-----EESQVLTVESLIMDKIYEDVKNESVPMRETVSIRK 129  
 DB 100 ee-eelpavaaesikvvaedklesseevlgde-----envegyklkadeptye----- 147  
 QY 130 ISKPRSPIDPPGSGRIYIDISLGFROHLDYRSQYKRLKEEDIKTSGIDAFSGYERF 189  
 DB 148 --dkprvlpdpdgqklyqldmlegfrnhldyrysefkmraaidqhegyladafstgye 205  
 QY 190 KFSRSETGITYREMAPGATWAALIGDFNMNPNADVYTONCEGWEIFLPNNADSGPP 249  
 DB 206 kfgtfsaegilyrewapagaalvvgdlnwppnadtmtreneyvvelslpnnadgsppa 265  
 QY 250 IPHGRVVKIRMDTSGNNDISIPAWIKFSYQAPGELPYNGIYYDPPEEKYVKNPQRPKRP 309

Db	Protein	Location/Qualifiers	Label	OTHER
266	1phgsgtvlmdcrpsgkds1rkwk1fvaqgdelprpnyg1ydpdpreeekyvfqhpqrkpr			
QY	310 KSLRIYESHVMSSTPEVITNTYANFDDVLPRIKRLGYNAYOLMAIDESHYVASFGEYHT			
Db	326 nslrlryeshshimsspepk1ctyanrtfdey1prkkl1gynaxqma1qeshysasfgyhvt			
QY	370 NFVYASRRGPRDDIKSLIDKANEGLGLVLMQIVTSHASHSTYMLDGLMMFGCTGCHFHSG			
Db	386 nlfapsrtfgrpedk1skidkanelg1lvmldvshasn1ldg1ngfdctbly1fhg			
QY	430 PRGHNMWMSRLFNYSWEVYRFLLSNARWMLDEYKFDGFRFDGYTSMTHTNGLOVDFT			
Db	446 prghnmwmsr1lfnyswev1ltnatwv1leeykfdg1rfdgvtlsmu1hng1qvalf			
QY	490 GNNVEFGVATVDVAVVYMLMLNDMTHIGLEPEAVTIGEDVSGMPTVC1PEVDGSGVGDYR			
Db	506 gnygeyfgfatvdvavv1ym1vnd1lmg1yprveav1gelevs1mp1fc1pvdqdgvgfdyr			
QY	550 LHAHVAVDKVVETIQKRDSDMKIGDIYHMLNLRMKLEKVCVSAESHDQALVGDKTIAPWLM			
Db	566 lhaevpdkv1ellkqsgdey1vmmgd1vht1cnrrwsek1cvtyaesh1dga1vgdkt1atwlm			
QY	610 DKMYOFPMLDPRSPRPLIDRCVALHKKMIRLTIGLIGEGEYLFNPMKNEFGHEWIDPRGD			
Db	626 dkmydfmd1dps1vpr1drg1al1hkm1rtv1mg1sggey1lntfme1tdfhpew1d1rpr			
QY	670 LHHPSGKFVYGNVSYSDCKRRFRFDGNSKHLRYHQMGEPDOAIQHLERAYGPMTSEHQYT			
Db	686 qslpnsgr1vprgm1y1dkcrr1rfd1gdady1ryhmg1efdg1amq1h1eeky1g1fms1eqy1			
QY	730 SRKREPRRIIVFGRGLVYVFNEMHTSSYSPYRGCLAKPEKTKYKIVLDSDDPLFFGFGRLS			
Db	746 srkneekkv1l1fgrgl1v1ftr1hmsney1fdyrgv1clpky1y1vdsd1g1f1g1sr1d			
QY	790 HDARHFSFEGWYDNRPRSPMYTPORTVVVALVED 825			
Db	806 hdaey1f1adp1hnd1r1p1ost1sy1tpr1ta1v1y1aled 841			
RESULT	8			
AAR93804	standard; Protein; 842 AA.			
XX	AAR93804;			
XX	03-MAR-1997 (first entry)			
XX	Class A starch branching enzyme (direct sequencing).			
XX	Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;			
XX	amylose; viscosity; potato.			
KW	Solanum tuberosum.			
OS				
XX				
FH	Key	Location/Qualifiers		
FT	Misc-difference 43	/label= OTHER		
FT	/note= "encoded by ambiguous codon"			
FT	Misc-difference 304	/label= OTHER		
FT	/note= "encoded by ambiguous codon"			
FT	Misc-difference 348	/label= OTHER		
FT	/note= "encoded by ambiguous codon"			
FT	Misc-difference 594	/label= OTHER		
FT	/note= "encoded by ambiguous codon"			
FT	Misc-difference 610	/label= OTHER		
FT	/note= "encoded by ambiguous codon"			
FT	Misc-difference 747	/label= OTHER		

Query Match	Similarity	73.2%	Pred. No. 1.3e-295;	Matches 606;	Conservative 85;	Mismatches 102;	Indels 35;	Gaps
189	stryemngftratrsgltlyrewapgsqsalgdfnwnadadimltnrefgweilfpnv	189	stryemngftratrsgltlyrewapgsqsalgdfnwnadadimltnrefgweilfpnv	189	stryemngftratrsgltlyrewapgsqsalgdfnwnadadimltnrefgweilfpnv	189	stryemngftratrsgltlyrewapgsqsalgdfnwnadadimltnrefgweilfpnv	189
185	sgcykrfegrsrengitryrenapgatmatalcgnnmnmnvdvntomdcgymeilefnpna	185	sgcykrfegrsrengitryrenapgatmatalcgnnmnmnvdvntomdcgymeilefnpna	185	sgcykrfegrsrengitryrenapgatmatalcgnnmnmnvdvntomdcgymeilefnpna	185	sgcykrfegrsrengitryrenapgatmatalcgnnmnmnvdvntomdcgymeilefnpna	185
129	lidesdrirerigipppqlygkrlieqldpiltlyrghldyrsyqkllrealdkyeggleat	129	lidesdrirerigipppqlygkrlieqldpiltlyrghldyrsyqkllrealdkyeggleat	129	lidesdrirerigipppqlygkrlieqldpiltlyrghldyrsyqkllrealdkyeggleat	129	lidesdrirerigipppqlygkrlieqldpiltlyrghldyrsyqkllrealdkyeggleat	129
133	-----kprstipprgcoritvdiplstfgrhondlyrsoykrleeridkylsgslidar	133	-----kprstipprgcoritvdiplstfgrhondlyrsoykrleeridkylsgslidar	133	-----kprstipprgcoritvdiplstfgrhondlyrsoykrleeridkylsgslidar	133	-----kprstipprgcoritvdiplstfgrhondlyrsoykrleeridkylsgslidar	133
69	tdvdsstmehsaqkltehdvpsadltgsvveeldfasslqlqgggkleeaklntseet	69	tdvdsstmehsaqkltehdvpsadltgsvveeldfasslqlqgggkleeaklntseet	69	tdvdsstmehsaqkltehdvpsadltgsvveeldfasslqlqgggkleeaklntseet	69	tdvdsstmehsaqkltehdvpsadltgsvveeldfasslqlqgggkleeaklntseet	69
98	tdveslindd-----kivedev-----nkessvprketyisirkigs-----	98	tdveslindd-----kivedev-----nkessvprketyisirkigs-----	98	tdveslindd-----kivedev-----nkessvprketyisirkigs-----	98	tdveslindd-----kivedev-----nkessvprketyisirkigs-----	98
9	knlslrklilaekssvnsesrstvtvaasgkvlvpxgdsdssstsdqdfetetspensps	9	knlslrklilaekssvnsesrstvtvaasgkvlvpxgdsdssstsdqdfetetspensps	9	knlslrklilaekssvnsesrstvtvaasgkvlvpxgdsdssstsdqdfetetspensps	9	knlslrklilaekssvnsesrstvtvaasgkvlvpxgdsdssstsdqdfetetspensps	9
39	keafsrarvsgkshedsdssnmvmtaskryl-pcgrlreccssgsrdoleapgtvsssoyvl	39	keafsrarvsgkshedsdssnmvmtaskryl-pcgrlreccssgsrdoleapgtvsssoyvl	39	keafsrarvsgkshedsdssnmvmtaskryl-pcgrlreccssgsrdoleapgtvsssoyvl	39	keafsrarvsgkshedsdssnmvmtaskryl-pcgrlreccssgsrdoleapgtvsssoyvl	39
72.8%	Score 3309.5;	DB 17;	Length 842;					
Best Local Similarity	73.2%	Pred. No. 1.3e-295;						
Matches 606;	Conservative 85;	Mismatches 102;	Indels 35;	Gaps				

QY 245 DGSPPPHSGRYKTRMDTSGNKDSTIPAMIKFSVOAGELPYNGIYDPPEEKYVFNK 304  
 DB 249 dgsppphsgryktrmdtsgnkdstipamikfsvoagelpyngiydppeekyvxftfp 308  
 QY 305 QPFRPKSLRTYSHGMSSTEPYINTYANFRDVLPRIKKIGYNAVQMAIOESHYASAF 364  
 DB 309 qpfrpkslrtysghmsstepynfntyanfrdvlprikkiqynavqmaioeshyaf 368  
 QY 365 GYHVTNFYVASSRFGTPDDLKSLIDKAHELGLVLMIDIVHSHASTNTDGLNMFDDG 424  
 DB 369 gyhvtnfassrfgtppddlkslidkahelglvlnmidivhshastntdglnmfddg 428  
 QY 425 YFHSRGGRHHMMWDSRLFNYSWGVYLRFLSNARKWMLDEYFDFGRDGVTSMMYTHHGL 484  
 DB 429 yfhsrggrhmmwdsrlfnyswgvylrflsnarkwmldeyfdgrdgvtsmmythhgl 488  
 QY 485 QVDFGNTNENYFGYATDVAVYLMILNDMTHGFEPEAVTIGEVSGMPYTCIVEGGV 544  
 DB 489 qvdfgntnenyfgyatdvavylmlndmthgfepeavtigevsgmptyctiveggv 548  
 QY 545 GEDYRLHMAVADKWEIIOKRDEDMKMDIVHMLNRRMLEKCVSYASHDQALVGDXTI 604  
 DB 549 gedylrhmaivadkweiiokrdedmkmdivhmlnrrmlekcvsyashdqlvgdxti 608  
 QY 605 AFWLADKMDYPMALDRPSTPLIDRGVALHMKIRLITMGLEGESTLMPKNGEFGHPWID 664  
 DB 609 afwladkmdypmaldrpstplidrgvalhmkirlitmglegestlmpkngfghpwid 668  
 QY 665 FPRGDLPLPSKFEVPGNNYSYDKCRFRDLGNSKHLRYHGMQOEQDAIOHLEAYGFMFS 724  
 DB 669 fprgdlplpskfevpgnnysydkcrfrdlgnskhlryhgmoeqdaiohleaygfmfs 728  
 QY 725 EHOYSRKDEDRILIVERGNTLVFVFNHTSSISIDRVGCLKPGKXKIVLSDSDPLFG 784  
 DB 729 ehoyrskdeedriliivergntlvfvfnhtssisidrvvgclkgkxkivlsdspdplfg 788  
 QY 785 FGRSLSHAENHPSFEGWYDNMRSPMYTTPCARTAVYALVYLVDEVEENLE 832  
 DB 789 fgrslshaenhpsfegwynydnmrspmyttpcartavyalvylvdeveenne 835

## RESULT 9

AAY06917  
 ID AAY06917 standard; Protein; 768 AA.  
 AC  
 AAY06917;

05-JUL-1999 (first entry)  
 DE  
 XX

Starch branching enzyme II (SBE II) amino acid sequence.  
 DE  
 XX

Starch biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBE; GBSS;  
 starch branching enzyme; starch soluble synthase; debranching enzyme;  
 endosperm; wheat; barley; granule-bound synthase; glutenin; starch;  
 grain softness protein I; bacterial isomylase; glycogen synthase;  
 WSB I-D4 gene.  
 KW  
 XX

Triticum tauschii.  
 OS  
 XX

MO914314-A1.  
 PN  
 XX

25-MAR-1999.  
 PD  
 XX

11-SEP-1998; 98WO-AU00743.  
 PF  
 XX

20-MAR-1998; 98AU-0002509.  
 PR  
 XX

12-SEP-1997; 97AU-0009108.  
 XX  
 XX

(CSTR) COMMONWEALTH SCI & IND RES ORG.  
 PA  
 (GOOD-) GOODMAN FIELDER LTD.  
 PA  
 (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.  
 (AUSU) UNIV AUSTRALIAN NAT.  
 XX

PI Li Z, Morell M, Rahman S;  
 XX  
 DR WPI; 1999-229525/19.  
 XX  
 PT New isolated cereal plant enzyme genes used for, e.g. expression of  
 PT antisense sequences of granule bound synthase  
 XX  
 PS Disclosure: Page 83-85; 171pp; English.  
 XX  
 CC The invention relates to a novel enzyme of starch biosynthetic pathway  
 CC in a cereal plant, where the enzyme is selected from starch branching  
 CC enzyme (SBE) I, SBE II, starch soluble synthase (SSS) I, and debranching  
 CC enzyme (DBE), with the proviso that the enzyme is not SSS I of rice, or  
 CC SBE I of rice or maize. The methods and products can be used for  
 CC targeting expression specifically to the endosperm of the seeds of cereal  
 CC plants such as wheat or barley. They can be used for the expression of  
 CC e.g. antisense sequences of granule-bound synthase (GBSS), SBE II, low  
 CC mol. wt. glutenin, grain softness protein I, bacterial isomylase,  
 CC bacterial glycogen synthase, and wheat high mol. wt. glutenin Bx17. They  
 CC can be used for modifying the characteristics of starch produced by a  
 CC plant. The present sequence represents the SBE II protein sequence.  
 CC  
 SQ Sequence 768 AA;

Query Match 71.3%; Score 3241.5; DB 20; Length 768;  
 Best Local Similarity 77.2%; Pred. No. 2,1e-289;  
 Matches 582; Conservative 78; Mismatches 83; Indels 11; Gaps 2;

QY 78 SSSIDQLRAPGTVEESQVLN-----DVESLIMDKIYEDVKNESYPMRETVSIRKI 130  
 DB 19 aaqpeelqipeedieaeaynmgttaeklessepqgvtelttdygvkxelv-----v 74  
 QY 131 GSKRSTIPPRGGRITDIDPSLGFROHLDYRSQYKRIREEIDKYEGSLDAFSRGYER 190  
 DB 75 gekprvpkpgdgqklyelpcltkdirshldryseyrriraaidqheggleafsfgyak 134  
 QY 191 FGFSRSETGILYRRMAGATMAALIGDFNNMNPADVMTONEGWEIETPLNNAAGSPRI 250  
 DB 135 lqftrsaeglitrewapghsaalvgdfinnpnadmtlctddgyvveltlpnadgspsal 194  
 QY 251 PHGSRVKTIRMDTPSGNKDSTIPAMIKFSVOAGELPYNGIYDPPEEKYVFNKPKRP 310  
 DB 195 phgsrvktirmdtpsgnkdstipamikfsvoagelpyngiydppeekyvxftfpkxpe 254  
 QY 311 SLRTYSHGMSSTEPYINTYANFRDVLPRIKKIGYNAVQMAIOESHYASFGYHVTN 370  
 DB 255 slrtysghmsstepynfntyanfrdvlprikkiqynavqmaioeshyafgyhvtn 314  
 QY 371 FYAASSRFGTPDDLKSLIDKAHELGLVLMIDIVHSHASTNTDGLNMFDDG 430  
 DB 315 fyassrfgtppddlkslidkahelglvlnmidivhshastntdglnmfddgldtbfhggp 374  
 QY 431 RGHMMWDSRLFNYSWGVYLRFLSNARKWMLDEYFDFGRDGVTSMMYTHHGLQVDTG 490  
 DB 375 rghmmwdsrlfnyswgvylrflsnarkwmldeyfdgrdgvtsmmythhglqvmftg 434  
 QY 491 NYNEFGYATDVAVYLMILNDMTHGFEPEAVTIGEVSGMPYTCIVEGGV 550  
 DB 435 nynefgyatdvavylmlndmthgfepeavtigevsgmptyctiveggvgtfvr 554  
 QY 551 HMAVADKWEIIOKRDEDMKMDIVHMLNRRMLEKCVSYASHDQALVGDXTI 610  
 DB 495 hmaivadkweiiokrdedmkmdivhmlnrrmlekcvsyashdqlvgdxtiafvlmd 554  
 QY 611 KDMYDFMALDRPSTPLIDRGVALHMKIRLITMGLEGESTLMPKNGEFGHPWID 670  
 DB 555 kdmxdfmaldrpstplidrgvalhmkirlitmglegestlmpkngfghpwidfprgq 614  
 QY 671 HLPSCGFVPGNNYSYDKCRFRDLGNSKHLRYHGMQOEQDAIOHLEAYGFMFS 730  
 DB 615 hlpsgfvpvgnnysydkcrfrdlgnskhlryhgmoeqdaiohleaygfmfsmsehyvs 674



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PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148365.
PR 13-AUG-1999; 99US-0148384.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150366.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158366.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 14-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 22-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Query Match 70.8%; Score 3219.5; DB 21; Length 721;  
 Best Local Similarity 81.5%; Pred. No 2e-287;  
 Matches 573; Conservative 66; Mismatches 61; Indels 3; Gaps 1;

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QY 135 RSTPPGKQRIYDIPSTIGFQRLADYRYSQYKRLREIDKESGLDAFSGYEFKFGFS 194
DB 12 Rklppgdkrlydipmshnmhldyrygykrlreidkneqgleafsfgyeflfgft 71

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QY 195 RSEFTITREMPAGATMAALIGDFNNMNPADVMTQNEGYEITFLPNMADGSPPIPHGS 254
DB 72 ratstgityrewagakaasllidfdnnnaksdmarndfgyweflppnadgsaiphgs 131
QY 255 RYKIRMDPTSSGNKDSIPAMIKFSVQAPGELPYNGIYDPEEERYKRNQPKRPSLR 314
DB 132 rtklrmtdcpsgikdsipawikysvpgpelpyngvvydpppeedkyatkhprrpktslrl 191
QY 315 YESHVGMSSTEEPIVNTYANFRDVLPRIKILGYNAVOLMIOESYASGCVHTNPNYA 374
DB 192 yeshvgmsstepekintynfrtdvlprikilgynavqimaqenayasygynvthflap 251
QY 375 SRRFGTPDDLKSLDKAHELGLVLMIDIVHSHASTNTLDGLNMFEDGDFHFGSPGRH 434
DB 252 ssrfgtpddlksldkahlglvlmidivhshaskntldglmdfdgdfgflnsgsrgyh 311
QY 435 WMMDSRLFNYSMEYLRLPLSNARWMLDEVKFDGFRRDGYTSMMYTHHGLQVDFGNVNE 494
DB 312 wmmdsrlfnysweylrplslsnarwmldeykdgfrfdgytsmmythhglqveflgnyne 371
QY 495 YFGYATDVDAVYYLMLNDMTIHGLFPAVTLIGEDVSGMPVCIPEBDGSGFPRRLHMAV 554
DB 372 yfgystdvdayymlndlmthglfpeavtligedvsgmpafcvpebdgsgfprlhmav 431
QY 555 ADKWEIIOKREDEMKMGDIYHMLTNRRLWLEKCVSAESHDAQLVGDKTIAFWLMDKMY 614
DB 432 adkweliiokredemkgdiyhmltnrrwlekcvsaseshdaqlvgdkctiafwlmdkmy 491
QY 615 DFMALDRSTPLIDRGVALHMKMLITMGISGEGYINFMKNEGHENIDFPRGLHLPS 674
DB 492 dfmaldrstplidrgvalhmkmlitmgisggyinfmkneghenidfprglhlps 551
QY 675 GKFPVGNNSYDKCRRFEDLGNSKHLRYHGMQEFDAIOLHEAYEFMTSEHOYSRKE 734
DB 552 gkfpvgnnsydkcrrfddlgdaeylryhglqefdamqnlleetygfmsehoysrke 611
QY 735 RDRITVEERGNLVFVFNHMTSSYSDYRVGCLPKGYKIVLSDDBLFSGFRLSHDAEH 794
DB 612 gdrivtergnllfvfnhmtssydyrvvgclpkgykivlssdblfsgfrrlshdaeh 711
QY 795 FSPFGWYDNRRPSFMVYTPCPTAVYALVEDEYENE---LEPV 834
DB 672 ftsdgrndrpscfmyaportavyaavdddddersslvpi 714

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RESULT 11  
 AAR60811 standard; Protein; 825 AA.  
 XX  
 AC AAR60811;

DT 05-JUL-1995 (first entry)

DE Rice starch branching enzyme.

KM Starch branching enzyme; rice; starch content.

OS Oryza sativa.

FN Key Location/Qualifiers

FT Peptide 1..65

FT Protein /label= transit-Deptide

PD 20-SEP-1994. /label= starch\_branching\_enzyme

PN JP06261767-A.

PF 22-OCT-1993; 93JP-0265171.

PR 29-OCT-1992; 92JP-0291719.

XX (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.  
 XX WPI: 1994-37418/42.  
 DR N-PSDB: AAO73750.  
 XX  
 PT New gene of branching enzyme of rice starch - useful for  
 PT increasing starch yield of rice grains  
 XX  
 PS Claim 1: Page 9-12; 13pp; Japanese.  
 XX  
 CC The rice starch branching enzyme (AAR60811) and cDNA encoding it  
 CC have been isolated. The starch content of rice grains can be  
 CC increased by increasing the expression of branching enzyme in  
 CC rice plants.  
 XX  
 SQ Sequence 825 AA:  
 Query Match 70.0%; Score 3180; DB 15; Length 825;  
 Best Local Similarity 70.3%; Pred. No. 1.1e-283;  
 Matches 586; Conservative 87; Mismatches 116; Indels 44; Gaps 7;  
 9 IREPCAPLCKSOSTGFHGYRTSCLSFNFKEAFSRVFSKSHESDSSVMYATAS--- 65  
 20 vrfpv-----pagarwraaaelp-----srlslsgrifpavrvvgsgqgavvraaas 70  
 66 -KRLPDGRLE-CYSSSTDQLEAPGVSE-----ESQVLNDESLLIMDKIVE 111  
 71 gevmlpegsdgmprvaasddqlpaldelslevgaevlessagsdvegv---krvv 126  
 112 DEVNKSVPARETVSIRKIGSKPRISIPPRGRORTYIDPSSLTGFRHLDIRYSQYKRLR 171  
 127 eelaae-----qkprvvpplcgdqkifgmmslmgkykhleryalsyrlr 172  
 172 EELDKYEGSLDARSRGKRGFSRSETGITYREMAFGATMALIDFNWNPNDVMTON 231  
 173 sdldqyegslsetsryekfgfhasegytyrewagghaalsaldvfnwmpndrmekn 232  
 232 ECGWTEIFPNMADGSPRPHGSRVKIRMDTPSGNKDSIPAWIKFSVQAPGLPYNGIY 291  
 233 eerywelfpnadgsaprlphgsrvrvmetpsgikdsipawikysvqagagipyngly 292  
 292 DPEEEKYVRKNQPKRKSLRTYESHVGMSSTEPYINTYANPRDVPRIKILGYNAVO 351  
 293 dpeeeekyrlkhpqpkrlrlyelclvngmsstepkinyanfrdevprliklgynavq 352  
 352 LMAIQEHSYASFGYHVTNFTYAASSRFGTPDDKSLIDKAHELGILYIMDIHSHASTNT 411  
 353 lmaiqehayysfgyhvtntfapsstfgpcedkslidakahelglvymdvshasnt 412  
 412 LDGILNMGDGDGHFHSGRPGHMMWDSRLFNTGSEVYLFELLSNARKWMLDEYKKGPRF 471  
 413 ldglingldgldthfhsgrgfhmmwdsrlfngsevrflfllsnarwaleeklogrlf 472  
 472 DGVTSMWYTHHGLOVDFTGNYNEFYGATVDVAVYLMILNDMIHGLFPBPAVITIGEDVG 531  
 473 dgytsmwythhglqvdfthgnynefygatyvdvavylmilmndmihglfpbpaavg 532  
 532 MPTVCIPVEDGGVGFEDRLHMAVADKWVEIIOKREDEDMKMGDIVHMLTNRMLERKCVSYA 591  
 533 mptvcipvedggvgfedyrlhmapvdkwlellkgsdeswmgdvlhcltnrrvsekcvtya 592  
 592 ESHOAVYGDKTIAFWLMDKMYOFMALDRSPFLIDRGVALHMKMLRLITMGISGEGYIN 651  
 593 eshoavlygdktiafwlmdkmyofmaldrspfldrgvalhmkmlrlitmgisggyin 652  
 652 FMGNFEGPEWIDPPRGDLHPSGKFPYGNVSYDCKRRRFPDIGNSHLHYHGMOFEDA 711  
 653 fmgnfegpewidpprgdlhpsgkfpynvsgydkrrrpfidgaddylyrygmlefda 712  
 712 IOHLEAVGFMTSEHOYISRDERDRIIVFRGNLWVYVFNFWHTSSYSDRVNCLKRGKX 771

Db 713 mgsleekyfmtdshgylsrkheedkmlilekgdlyfvfnfmsnyfydyvgc:kpkgy 772  
 Qy 772 KIVDSDPLEGFGGRSLSHDAEHFSEGWYDNRPSFMYTTPCRNAVYALVE 824  
 Db 773 kvvldsaglfgyfgrlhtaetfadcshndrpfysfyspaltcvyapae 825

## RESULT 12

AAW70895  
 ID AAW70895 standard; protein; 871 AA.

AAW70895;  
 23-AUG-1999 (first entry)

Maize branching enzyme II.

Non-glycogen-like polysaccharide production; fermentation;  
 starch synthesis enzyme; glycogen-synthesis enzyme; glycogen synthesis;  
 non-starch branching gene; amylopectin; amylose; plant-like starch;  
 maize branching enzyme II.

Zea mays.

MO9844780-A1.

15-OCT-1998.

03-APR-1998; 98WO-US06660.

04-APR-1997; 97US-0042939.

(EXSE-) EXSEED GENETICS LLC.

Guan H, Keeling PL;

WPI: 1998-568285/48.

N-PSDB: AAW70361.

Producing non-glycogen-like polysaccharides in bacteria, fungi or  
 plants - transforming with genes for enzymes involved in starch or  
 glycogen synthesis allows fermentative production of starches with  
 engineered properties

Disclosure; Fig 53; 150pp; English.

The specification describes a method for the production of  
 non-glycogen-like polysaccharides in a host. The method comprises  
 transforming a host, suitable for fermentation, with genes encoding  
 starch- or glycogen-synthesis enzymes, and fermenting the transformants.  
 The specification also describes hosts transformed with a gene active  
 in glycogen synthesis and at least one non-starch branching gene,  
 involved in production of amylopectin or amylose in its original host.  
 The method is used to produce plant-like starches for fermentation and  
 new starches in plants. These starches are useful for all food and  
 non-food applications of starch. The present sequence is used in  
 the course of the invention.

Sequence 871 AA:

Query Match 69.7%; Score 3169; DB 19; Length 871;  
 Best Local Similarity 70.4%; Pred. No. 1.2e-282;  
 Matches 584; Conservative 84; Mismatches 93; Indels 68; Gaps 8;  
 2 GHYITSGIRPPCAPLCKSOSTGFHGYRTSCLSFNFKEAFSRVFSKSHESDSSVMY 61  
 33 glftrgavgc-----sghngamraa-----aaarka-----vm 62  
 Db 62 VTASKRVLPDG---RIECYSSSTDQLEAPGVSEBQV---LTDVSLIMDKIYEDVEN 115  
 Qy 63 vpegen---dglasradsaqfqsdelevp-disetlcgagvadaqal----- 106

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QY 116 KESVPMRETSIRKIGSKRSIPPPGQRIYDIDPSLTGFRQHLDYKSYQKRLREID 175
DB 107 -----nrvtyvppsdgqkifidpmlqgkykylleyrslrrlridid 150
QY 176 KYEGSLDAFSRGEKFGESRSETGITYREMAFGATMAALIDGFNNMNPADVMQNECGV 235
DB 151 ehaggleatrsyefgfnraaeqilyrewapgaftsaalvgdlnwppndmrsknefyv 210
QY 236 WEIFLPNNADSPPIPHGSRVKIRMDTPSGNKSIPANIKFSVOAPGELPNNGIYDPE 295
DB 211 weiflpnnadgtsplphgsrvkvrmdtpsglkdslpawlkysvqapgeipydilydppe 270
QY 296 EEKYVFKNPQKRRKSLRIYESHVGMSTEPYINTYANFRDVLPRIKKLGNVQMLAI 355
DB 271 evkyyfirhaqpkrrkslriyethygmsspepkintynfridevlprikklgynaavqlmai 330
QY 356 QEHSYVASFGEYHNTNFYAASRFGTDDLSLIDKAHEGLGLVLMQDVHSHASTNTDGL 415
DB 331 qehsyysfgyhvntnfafpsrftgpeelnsldraheglglvldvshassntldgl 390
QY 416 NMFDGTHGFHSRGRGHMMWDSRLFNYSWEVLRFLSNARWMLDEYKFRDFDGYT 475
DB 391 ngfdgthghfhsgrghmmwdsrlfngynwevlfllsnarwleeykfrdfgdyt 450
QY 476 SMATYTHGLQVDFGTGNTEYFGYATDVAVYYLMLNDMTHGLFPEAVTIGEDVSGMPTV 535
DB 451 smatythnglqvtfgntheeyfgfatdvavyylmvndlthglfpeavtlgedvsgmptf 510
QY 536 CIPVEDGCVGFYRLHMAVADKWELIQRDEBWKMGDIYHMLTNRRWLEKCVSYAESHD 595
DB 511 alpyhdggvgfydrrmhnavaekwidllkgsdetwkmgdvlnltnrrwlekyvyaeshd 570
QY 596 QALVGDKTIAFWLMDKMYDFMALDRPSTPLIDRGVALHKMIRLITMGLEGEGYLNMGV 655
DB 571 qalvgdktiafwlmdkmydfmaldrpstplidrgvalhkmirlitmgleggylnmgv 630
QY 656 EFGFEMIDPPRGDLH.PSGKFPVGNMYSYDKORRRPDLGNSKHLKRGHQEDQAIQHL 715
DB 631 efgfemidpprgdlhpsgkflpgnmysydkcrrtdlgdadylythgqefdgamql 690
QY 716 BEAVGEMTSEHOYISRKEDRRIIVERGNLVEVFNEHMTSSYSDYRVCGLKRGKYIVL 775
DB 691 ekygelmtdshqyisrkedrriiveergnlvevfnehmssysdyrvcgclrgkyivl 750
QY 776 DSDDPLEFGGGRSLSHAENHSEFGMTDNRRPSRMVYTPCTTAAVVALVE 824
DB 751 dsdapplfggrslshaenhsefgmtdnrrpsrmvytpcttaavvalve 799

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## RESULT 13

AAW56489  
ID AAW56489 standard; Protein; 799 AA.

AAW56489;

11-SEP-1998 (first entry)

DE Zea mays starch branching enzyme II.

KW SER; starch-encapsulating region; fusion vector;  
starch branching enzyme II; glucosyl transferase.

OS Zea mays.

PN WO9814601-A1.

PD 09-APR-1998.

PF 30-SEP-1997; 97WO-US17555.

PR 30-SEP-1996; 96US-0026855.

PA (EXSE-) EXSEED GENETICS LLC.

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XX
PI Guan H, Keeling P.
DR WPI, 1998-240100/21.
DR N-PSDB; AAV29757.
PT Hybrid polypeptide comprising starch-encapsulating region and
PT protein - useful for, e.g. producing protein(s) resistant to
PT degradation by stomach acids
PS Example 2; Page 43; 156pp; English.
XX
CC The sequence is that of starch branching enzyme II.
CC It can be used in the production of a hybrid polypeptide
CC comprising a starch-encapsulating region (SER) fused
CC to a payload protein. The hybrid polypeptide can be used to make
CC modified starches comprising the payload protein, selected from,
CC e.g. hormones, growth factors, antibodies, enzymes, dyes,
CC immunoglobulins, etc. The modified starch can also be used
CC to provide grain feeds enriched in amino acids. By encapsulating
CC the payload protein in starch, it is more resistant to
CC degradation by stomach acids.
XX
SQ Sequence 799 AA:

```

## Query Match

Best local similarity 70.3%; Score 3160; DB 19; Length 799;  
Matches 583; Conservative 83; Mismatches 95; Indels 68; Gaps 8;

```

QY 2 GHATYIGIRFPAPLCKSOSTGFHGYRRTSCLSFNFKEAFRRYFSGSKSHEDSSNMV 61
DB 33 glflltrgavgc-----sgthgamraa-----aaarka-----vm 62
QY 62 YIASKRVLDG---RECYSSSTDQLEAPGVSESYQV---LTVESLIMDKIVEENV 115
DB 63 vpegen---dgiasradsqfsgdelevp-diseetcgayadagal----- 106
QY 116 KESVPMRETSIRKIGSKRSIPPPGQRIYDIDPSLTGFRQHLDYKSYQKRLREID 175
DB 107 -----nrvtyvppsdgqkifidpmlqgkykylleyrslrrlridid 150
QY 176 KYEGSLDAFSRGEKFGESRSETGITYREMAFGATMAALIDGFNNMNPADVMQNECGV 235
DB 151 ehaggleatrsyefgfnraaeqilyrewapgaftsaalvgdlnwppndmrsknefyv 210
QY 236 WEIFLPNNADSPPIPHGSRVKIRMDTPSGNKSIPANIKFSVOAPGELPNNGIYDPE 295
DB 211 weiflpnnadgtsplphgsrvkvrmdtpsglkdslpawlkysvqapgeipydilydppe 270
QY 296 EEKYVFKNPQKRRKSLRIYESHVGMSTEPYINTYANFRDVLPRIKKLGNVQMLAI 355
DB 271 evkyyfirhaqpkrrkslriyethygmsspepkintynfridevlprikklgynaavqlmai 330
QY 356 QEHSYVASFGEYHNTNFYAASRFGTDDLSLIDKAHEGLGLVLMQDVHSHASTNTDGL 415
DB 331 qehsyysfgyhvntnfafpsrftgpeelnsldraheglglvldvshassntldgl 390
QY 416 NMFDGTHGFHSRGRGHMMWDSRLFNYSWEVLRFLSNARWMLDEYKFRDFDGYT 475
DB 391 ngfdgthghfhsgrghmmwdsrlfngynwevlfllsnarwleeykfrdfgdyt 450
QY 476 SMATYTHGLQVDFGTGNTEYFGYATDVAVYYLMLNDMTHGLFPEAVTIGEDVSGMPTV 535
DB 451 smatythnglqvtfgntheeyfgfatdvavyylmvndlthglfpeavtlgedvsgmptf 510
QY 536 CIPVEDGCVGFYRLHMAVADKWELIQRDEBWKMGDIYHMLTNRRWLEKCVSYAESHD 595
DB 511 alpyhdggvgfydrrmhnavaekwidllkgsdetwkmgdvlnltnrrwlekyvyaeshd 570
QY 596 QALVGDKTIAFWLMDKMYDFMALDRPSTPLIDRGVALHKMIRLITMGLEGEGYLNMGV 655
DB 571 qalvgdktiafwlmdkmydfmaldrpstplidrgvalhkmirlitmgleggylnmgv 630

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62 VTASKRVLPDG---RIECYSSSTDQLEAPGVSEESQV---LIDVES

PF 25-FEB-2000; 2000EP-0301439

XX 3E-FFD-2000. 2000FB-0301439



PR 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128233.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 23-APR-1999; 99US-0130891.  
PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 06-MAY-1999; 99US-0132487.  
PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137528.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139453.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 21-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 28-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.

PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
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PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
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PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
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PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
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PR 04-OCT-1999; 9905-0157117.  
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PR 28-OCT-1999; 9905-0161920.  
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Best Local Similarity 69.1%; Score 3140.5; DB 21; Length 693;

Matches 559; Conservative 65; Mismatches 58; Indels 3; Gaps 1;

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OM protein - protein search, using sw model

Run on: August 7, 2001, 11:14:23 ; Search time 14.01 Seconds  
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Searched: 197339 seqs, 20590346 residues

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Maximum Match 100%  
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28: /cgn2\_6/ptodata/2/1aa/6Z.COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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4	2124	46.7	822	3	US-08-941-445A-17
5	1635.5	36.0	566	4	US-08-104-158-2
6	542.5	11.9	652	4	US-08-528-026C-4
7	232.5	5.1	606	4	US-09-187-124-2
8	226	5.0	325	4	US-08-961-083-80
9	224.5	4.9	589	1	US-08-399-646-2
10	224.5	4.9	589	1	US-08-607-321-2
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13	224.5	4.9	589	2	US-08-399-646-12
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27	217	4.8	556	2	US-08-505-377-1

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## ALIGNMENTS

RESULT 1  
US-09-087-277-2  
; Sequence 2, Application US/09087277B  
; Patent No. 6169226

GENERAL INFORMATION:

APPLICANT: EK, Bo  
APPLICANT: KHOSNODI, Jamshid  
APPLICANT: LARSSON, Clas-Tomas  
APPLICANT: LARSSON, Hakan  
APPLICANT: RASK, Lars

TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO  
FILE REFERENCE: 003300-486

CURRENT APPLICATION NUMBER: US/09/087, 277B

EARLIER FILING DATE: 1998-05-29

EARLIER APPLICATION NUMBER: PCT/SE96/01558

EARLIER FILING DATE: 1996-11-28

EARLIER APPLICATION NUMBER: SE 9504272-7

EARLIER FILING DATE: 1995-11-29

EARLIER APPLICATION NUMBER: SE 9601506-0

EARLIER FILING DATE: 1996-04-19

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 878

TYPE: PRT

ORGANISM: Unknown

FEATURES:

OTHER INFORMATION: Description of Unknown Organism:bell gene (branching enzyme II

US-09-087-277-2

Query Match

Best Local Similarity 74.5%; Score 3387.5; DB 4; Length 878;

Matches 621; Conservative 92; Mismatches 116; Indels 35; Gaps 5;

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63 TASKRVL-PDGRTECYSSSTDLQAPGVSESOVLTVESLIMD---RIVEDEV--- 114

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us-09-297-703a-29.ra1

Page 2

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RESULT 2  
US-08-941-445A-15  
Sequence 15, Application US/08941445A  
Patent No. 6107060  
GENERAL INFORMATION:  
APPLICANT: Keeling, Peter  
APPLICANT: Guan, Haining  
TITLE OF INVENTION: Starch Encapsulation  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
STREET: 5370 Manhattan Circle  
CITY: Boulder  
STATE: CO  
COUNTRY: US  
ZIP: 80303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/941,445A  
FILING DATE: 30-SEP-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/026,855

FILING DATE: 30-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Winner, Ellen P  
REGISTRATION NUMBER: 28,547  
REFERENCE/DOCKET NUMBER: 89-97  
TELEPHONE: (303) 499-8080  
TELEFAX: (303) 499-8089  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 799 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-941-445A-15

Query Match 69.5%; Score 3160; DB 3; Length 799;  
Best Local Similarity 70.3%; Pred. No. 2,4e-299; Mismatches 95; Indels 68; Gaps 8;  
Matches 583; Conservative 83; Mismatches 95; Indels 68; Gaps 8;

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631 EFGHEWIDFPRGDLHPSGKFPVNNYSYDKCRRRFDIGNSKRLRYGMOFDOALH 690  
716 EEAAGFMTSEHOYSRKRDEDRIRIYFEGNLYFVFNFWHTSSYSDYRVCGLKFGKIYV 775  
691 EEAAGFMTSEHOYSRKRDEDRIRIYFEGNLYFVFNFWHTSSYSDYRVCGLKFGKIYV 750

QY 776 DSDPLFGGRLSHDAHEFSEGWYNNRPSRSMVYTPCRTAVYALVE 824  
 DB 751 DSDAGLFGGFSRIHHAHEFTADCSHDNRPSFSVYTPSRCTCYAYAVE 799

## RESULT 3

US/09/087  
 ; Sequence 4, Application US/09087277B  
 ; Patent No. 6169226  
 ; GENERAL INFORMATION:  
 ; APPLICANT: EK, Bo  
 ; APPLICANT: KHOSNODI, Jamshid  
 ; APPLICANT: LARSSON, Clas-Tomas  
 ; APPLICANT: LARSSON, Hakan  
 ; APPLICANT: RASK, Lars  
 ; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO  
 ; FILE REFERENCE: 003300-486  
 ; CURRENT APPLICATION NUMBER: US/09/087, 277B  
 ; EARLIER APPLICATION NUMBER: PCT/SE96/01558  
 ; EARLIER FILING DATE: 1996-11-28  
 ; EARLIER APPLICATION NUMBER: SE 9504272-7  
 ; EARLIER FILING DATE: 1995-11-29  
 ; EARLIER APPLICATION NUMBER: SE 9601506-0  
 ; EARLIER FILING DATE: 1996-04-19  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 4  
 ; LENGTH: 464  
 ; TYPE: PRT  
 ; ORGANISM: Unknown  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Unknown Organism: be11 gene fragment (branching enz  
 US/09/087, 277-4

Query Match 48.5%; Score 2204; DB 4; Length 464;  
 Best Local Similarity 84.0%; Pred. No. 2e-206;  
 Matches 389; Conservative 40; Mismatches 34; Indels 0; Gaps 0;

QY 240 LPNNADGSPPIPHGSRVKTMDTPSGNKSIPAMIKFSVQAPGLPYNGIYDPPEEKY 299  
 DB 1 LPNNVDSGSPPIPHGSRVKTMDTPSGNKSIPAMIKFSVQAPGLPYNGIYDPPEEKY 60  
 QY 300 VFNPPQPKRKSLRIYSHVGMSTBPVINTYANFRDVLPRIKLGYNAVOLMAIOEHS 359  
 DB 61 IFQHPKPKRKSLRIYSHVGMSTBPVINTYANFRDVLPRIKLGYNAVOLMAIOEHS 120  
 QY 360 VYASFGYHTNFAAASRPGTDPDLKSLIDKAHEGLVLMDIVHSHASTNTLDGINMFD 419  
 DB 121 VYASFGYHTNFAAASRPGTDPDLKSLIDKAHEGLVLMDIVHSHASTNTLDGINMFD 180  
 QY 420 GIDGHHYHSGPRGHMMWMDSRLEFYNGSWELRFLSNARWMLDEYKFDGFRDGYTSNMY 479  
 DB 181 GIDGHHYHSGPRGHMMWMDSRLEFYNGSWELRFLSNARWMLDEYKFDGFRDGYTSNMY 240  
 QY 480 THHGLOVDTGNTNVEFYATDVDAVYVYMLNDMHLGFPFAVYTIAGEVSGMPYVCIYV 539  
 DB 241 THHGLOVDTGNTNVEFYATDVDAVYVYMLNDMHLGFPFAVYTIAGEVSGMPYVCIYV 300  
 QY 540 EDGCVGFYDLHMAVADKWEIIOKREDMKMGDIYHMLTNRWLEKCVSYASHDQALY 599  
 DB 301 EDGCVGFYDLHMAVADKWEIIOKREDMKMGDIYHMLTNRWLEKCVSYASHDQALY 360  
 QY 600 GDKTAFMLADKMDYDMLADRPSTPLIDRGVALHMKMIRLITMGLGEGYILNFMNGEFGH 659  
 DB 361 GDKTAFMLADKMDYDMLADRPSTPLIDRGVALHMKMIRLITMGLGEGYILNFMNGEFGH 420  
 QY 660 PEKIDFPRGDLHPSGKFPVGNYSYDKRRRFDLGNCSHLRY 702  
 DB 421 PEKIDFPRGDLHPSGKFPVGNYSYDKRRRFDLGNCSHLRY 463

## RESULT 4

US-08-941-445A-17  
 ; Sequence 17, Application US/08941445A  
 ; Patent No. 6107060

; GENERAL INFORMATION:  
 ; APPLICANT: Keeling, Peter  
 ; APPLICANT: Guan, Hanning  
 ; TITLE OF INVENTION: Starch Encapsulation  
 ; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
 ; STREET: 5370 Manhattan Circle  
 ; CITY: Boulder  
 ; STATE: CO  
 ; COUNTRY: US

ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/941,445A  
 FILING DATE: 30-SEP-1997  
 CLASSIFICATION: 800

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/026,855  
 FILING DATE: 30-SEP-1996

ATTORNEY/AGENT INFORMATION:  
 NAME: Winner, Ellen P  
 REGISTRATION NUMBER: 28,547

REFERENCE/DOCKET NUMBER: 89-97  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (303) 499-8080  
 TELEFAX: (303) 499-8089

INFORMATION FOR SEQ ID NO: 17:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 822 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-941-445A-17

Query Match 46.7%; Score 2124; DB 3; Length 822;  
 Best Local Similarity 56.1%; Pred. No. 3.4e-198;  
 Matches 389; Conservative 112; Mismatches 167; Indels 26; Gaps 6;

QY 146 IYDIDPSLTGRHLDIYRYSOYKRLREIDRYEGSLDAFSRGYKFGFSRSETGITYREW 205  
 DB 84 IYDIDPSLTGRHLDIYRYSOYKRLREIDRYEGSLDAFSRGYKFGFSRSETGITYREW 143  
 QY 206 APGATWALIDGPNWNNADVPMONCEGWEIFLPNNADGSPPIPHGSRVKTMDTPSG 265  
 DB 144 APGATWALIDGPNWNNADVPMONCEGWEIFLPNNADGSPPIPHGSRVKTMDTPSG 202  
 QY 266 NKDSIPAMIKFSVQAPGL--PYNGIYDPPPEEKYFKNPQPKRKSLRIYSHVGMSS 323  
 DB 203 NKDSIPAMIKFSVQAPGL--PYNGIYDPPPEEKYFKNPQPKRKSLRIYSHVGMSS 262  
 QY 324 TEPVINTYANFRDVLPRIKLGYNAVOLMAIOEHSYASFGYHTNFAAASRPGTDPDL 383  
 DB 263 TEPVINTYANFRDVLPRIKLGYNAVOLMAIOEHSYASFGYHTNFAAASRPGTDPDL 322  
 QY 384 LKSLIDKAHEGLVLMDIVHSHASTNTLDGINMFD--GTDGHHYHSGPRGHMMWMDSR 440  
 DB 323 LKSLIDKAHEGLVLMDIVHSHASTNTLDGINMFD--GTDGHHYHSGPRGHMMWMDSR 382  
 QY 441 LFNYSWSEVLRFLSNARWMLDEYKFDGFRDGYTSNMYTHHGLOVDTGNTNVEFYAT 500  
 DB 383 LFNYSWSEVLRFLSNARWMLDEYKFDGFRDGYTSNMYTHHGLOVDTGNTNVEFYAT 442  
 QY 501 DVDAVYVYMLNDMHLGFPFAVYTIAGEVSGMPYVCIYVDEGCVGFYDLHMAVADKWE 560

**Tue Aug 7 20:32:51 2001**

us-09-297-703a-29.rai

Page 4

Db	443	AVDVRVYVMMILANHHMLLEPAATVAVDVGSMPLCPRVDEGGGFGFDYRLAMAIPRWID	5020
Qy	561	IIOKRDE-DWKMGDIVHMLNRRHLECVSAESHDDALVGDGTIAFWLMDKMYDFMAL	619
Db	503	YLKKDDSEWMSGELATLTNRRRTETCKIYAESHDSIYGDKTIALLMDKMYGMSD	5620
Qy	620	DREPTPLIDRVAALAHKHTILRTLMOLGEGYLFNFGNEFGHPWIDPBGDLHLPSGKEVP	679
Db	563	LQPSPTPIDRQIALQKMIHFTYALAGDGYLNFNGNEFGHEWIDPFR-----E	611
Qy	680	GNNNSYDCRRRFPDLGNSKHLRYMGMOEFDQIDHLEAVGEMTSEHOYISRDERDRII	7399
Db	612	GNNNSYDCRCROWSLVPTDHLRTYRYMNAFDAMNALDERSEFLSSKOIYSDMNDKEKVI	671
Qy	740	VFERQNTLFEVFNFWHTSSYSDYRVGCLCKPGKXYKIVLDSDDLFCGFPRLSHDHEHSEF--	797
Db	672	VFERQDILFEVFNHPKRTYEGYKKGCDLPGKYRYALLDSDALVFGGHRVGGHDVHTSPE	733
Qy	798	-----EGWYDNRPRSEWYVTPCRTAVYALYED	825
Db	732	GVPGVPEFTENNRRPSEFVLSPPRTCAIYRYDE	765

RESULT 5  
 US-08-104-158-2  
 Sequence 2, Application US/08104158  
 Patent No. 6215042  
 GENERAL INFORMATION:  
 APPLICANT: Willmiller, Lothar  
 APPLICANT: Sonnenswald, Jens  
 APPLICANT: Kossmann, Jens  
 APPLICANT: Mueller-Roeder, Bernd  
 APPLICANT: Visser, Richard Gerardus Franciscus  
 APPLICANT: Jacobsen, Evert  
 TITLE OF INVENTION: PLASMIDS CONTAINING DNA-SEQUENCES THAT  
 TITLE OF INVENTION: CAUSE CHANGES IN THE CARBOHYDRATE CONCENTRATION AND THE  
 TITLE OF INVENTION: CARBOHYDRATE COMPOSITION IN PLANTS, AS WELL AS PLANT CELLS  
 TITLE OF INVENTION: AND PLANTS CONTAINING THESE PLASMIDS  
 NUMBER OF SEQUENCES: 2  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen  
 STREET: 1180 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036-8403  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/104,158  
 FILING DATE: 13-AUG-1993  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: EP PCT/EP92/00302  
 FILING DATE: 11-FEB-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: DE P 41 04 782.6  
 FILING DATE: 13-FEB-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Weilmund, Edward A.  
 REGISTRATION NUMBER: 34,735  
 REFERENCE/DOCKET NUMBER: RA-1996 PCT (951-91)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-382-0700  
 TELEFAX: 212-362-0888  
 TELEX: 236925  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 566 amino acids

```

;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-08-104-158-2

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Query Match	36.0%;	Score 1635.5;	DB 4;	Length 556;
Best Local Similarity	52.2%;	Pred. No. 8.7e-151;		
Matches 316; Conservative	89;	Mismatches 151;	Indels 49;	Gaps 9

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0Y 57 SNNWVATSKVLEVDGRIECSSTSSSTDLQVAVSSESVLEIVESLIMDOKVJ30EVRK 11
Db 4 SMDISSTFKSHVRDERMK-HSSALD-----SAVLTD-----DNS 36
0Y 117 ESVPREPVISRKIGSKPRSIPEPGRCORATYDIDPSLTGFRQHLIDYR5QYKRRLREEDIK 176
Db 37 TMAPLEEDVNTENIG-----LLNDLPTEPLEYDHFHRBMKRYVOQKMLIEK 82
0Y 177 YEGSLDAFSRGYERKFGPSRSTGTIYERMAPGAWMALIDFNWNNMNAVUMQNEGVW 236
Db 83 YEGPLEEPAQGLTKFGEFKREDGCIYTERMAPAOEALEYIGDFNCRGNSNHMMERK DQFGVW 142
0Y 237 ELFLPNMADGSPRIPIHGSRAKIRMDTPSGN-KDSIPAMIKF5VQAPGEL--PYN3IYTPD 293
Db 143 STRIP-DVDSKRVIPHNRSVRKFKHCGGWVDDIPIMIKATADATKPAAPD5YVMDP 201
0Y 294 PEEKEYVRKNPOPKRPSRLRIYESHVGSSTEPYINTYANFERDVLRIKKLGYNAVOM 333
Db 204 PSEYEHKRYPPRPAPRPIYEAHVGSSESPYVNSREFADVDYLRIRKANNNTYOLM 261
0Y 354 ATOESYVAFCEYHNTYNTVYVAA5SRFGYRDDKSLIDKANHGLGLVYLDIYH5HA5TNTLD 413
Db 262 ALMH5TYGSGEYHVTNTPFAVNSNRGNEDEDLKYLIDKANSGLQVLVDVYH5SHASNTVD 321
0Y 414 GJNMND---GTDGHNH5GPRGHHMMDSRLFN5NG5WEVLEFLLSNARWMLDEKFKDGF 470
Db 322 GJNGDIDIGOGS0ES5FHAG5RGYHKLMD5RLFNANNEVLEFLLSNARWMLDEEYNPF0GFR 381
0Y 471 FPGVTSAMATHHGLQVDTGANTNEFGATVQVDAVYUMLLMDHIGLFRPAVJ IGD5VS 530
Db 382 FPGTISMLTVHNGHIMGTGTGANTNEFSATDVAVYUMLNLINKHIFRPAVJ IAD5VS 441
0Y 531 GMPYTCIPYEDG5GVEDYRLAHNAVADKWEIYQ-KRDEKMGDIYHMLTYNRKRL5C5S 589
Db 442 GMPGSR5P5SEBGID5FYDRLAMAIYDKWIDYLLKNNDEMD5MKEVTSLSLNRRI TEKCIA 501
0Y 590 YAESHOQALVYGKTIATFAMLMDKMDYFALDRPSTPLIDRGSVALHMKIRLITMCLIG5EGY 649
Db 502 YAESHOQSLVYGKTIATFLMKNK5EYSGMSCLTDP5PVADGAIALDKMIFHFNCLIGRGV 561
0Y 650 LNFMG 654
Db 562 POEHG 566

```

RESULT 6  
 US-08-528-026C-4  
 ; Sequence 4, Application US/08528026C  
 ; Patent No. 6248566  
 ;  
 ; GENERAL INFORMATION:  
 ;  
 ; APPLICANT: IMANKA, Tadayuki  
 ; APPLICANT: TERADA, Yoshinobu  
 ; APPLICANT: TAKAHARA, Takeshi  
 ; APPLICANT: YAMASE, Michiyo  
 ; APPLICANT: OKADA, Shigetaka  
 ; APPLICANT: TAKATA, Hiroki  
 ; APPLICANT: NAKAMURA, Hiroyasu  
 ; APPLICANT: FUJII, Kazutoshi  
 ;  
 ; TITLE OF INVENTION: GLUCAN HAVING CYCLIC STRUCTURE AND METHOD FOR PRODUCING THE  
 ; FILE REFERENCE: 9900-0002.20  
 ; CURRENT APPLICATION NUMBER: US/08/528,026C  
 ; CURRENT FILING DATE: 1995-09-13  
 ; PRIOR APPLICATION NUMBER: US 08/415,152

PRIOR FILING DATE: 1995-03-31  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO.4  
LENGTH: 652  
TYPE: PRT  
ORGANISM: Bacillus stearothermophilus (Strain TRBEL4)  
US-08-528-026C-4

Query Match 11.9%; Score 542.5; DB 4; Length 652;  
Best Local Similarity 27.4%; Pred. No. 5.5e-44;  
Matches 192; Conservative 86; Mismatches 222; Indels 201; Gaps 32;

177 YEGSLDPAKSGYKFGF---SRSETGITYREWAPGATWAAALIGDENNNPNADVMTQ-- 230  
15 HEGSL---YKSYELFGAHYINBEGKYGTRFCVAPAHAREVLVGSNDMD-GTDFLELV 70  
231 NEGVWEILPNNADGSPPIHGSRYKIRMDPFGSKNKSIPAMIKFSVQAPGELPY---- 286  
71 NDEGVVTIYVPEMLR-----GHLKYKEIVTPDQ-----VLEKAD-----PYAFYS 111  
287 -----NGIYDPEEKEKYFNKPQKRPKSLR-----YESHYG-MSSTEPVINTY 331  
112 ELRPHTASTAID---LKGQWMDQSWKRRKRRRIYDQPMVITELHFGSWKKKDGREYTY 168  
332 ANFRDVLPRIKKIGYNAVOLMAIOESHYASFGYHVTNFAASRFGPDLLKSLIDKA 391  
169 REMADLLIYVLDHGTTHIELPLVPHPLDRSMGYGCTGYAVTSKYGIPHPMYFVDRC 228  
392 HELGLVLMIDYHSHASTYTLGLNFDGTDGHEHSGRHHMMWSLSLFNYGSEVLR 451  
229 HQAGIVINDWVPGHCKDA-HGLYMFDPAPTYEYANEKDRBNYVWGTANFLGKPEVRS 287  
452 FLISNARWMLDEKKEPGEFPGDVTSMYTHHGLQVDFGNTNMEYCYATDVAVYIMLL 511  
288 FLISNARWMLDEKKEPGEFPGDVTSMYTHHGLQVDFGNTNMEYCYATDVAVYIMLL 511  
512 NDMLHGLPEAVTIGEDVSGMPTVCIPVEDGCVGDFRILHMAVADKWEIIOKREDNMK 571  
336 NEAVFYDNDNALMIEDSDWMDPKYAPTEGGLGFNYK-----NNM 376  
572 GDIVHMLT-----NRMLEKCV-----SYAE-----SHDQALVGDKTAFVLMKD 612  
377 GMMNDMLKMYETPRYERRHVNQVTFSLIYAXSENFILPFSHDEYVHGKSL----- 428  
613 MYDMALDPRSTPLIDRGVALHKM-----IRLITMGLGEGY-----LNTWG 654  
429 -----LTKMPGSEYEKFAQLRLT-----YGYMAHPGKKLLEMG 462  
655 NEFGH-PEW-----IDPPRGDILHPSGKFPVGNNSYD-KCRRRPDLGSKHLR 701  
463 NEFAQDEKKEFDELDMWLFDF---ELHRKM-----NDYMKELLAC-----YKR 503  
702 YHGMQFDQALDHL- -EAYGFMTEHGYISKRDERLITVERGNLVEFNFHTSSYS 759  
504 YKPFYELDHDPOGFWMIDVHNAEQSIFSRIRGKKEDV-----LYVCFN-INQAYD 555  
760 DYRVGCIKRGKKIYLDSDPLFEGFG-----RLSHDAEHF 795  
556 DYKVGPLLVPRYREVLSNDVATFGSGHVGKRLSAFNEPF 596

RESULT 7  
US-09-187-124-2

Sequence 2, Application US/09187124A  
Patent No. 6255563  
GENERAL INFORMATION:  
APPLICANT: Emmermann, Michael  
APPLICANT: Kossmann, Jens  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES CODING FOR DEBRANCHING ENZYMES  
FILE REFERENCE: GFB8

CURRENT APPLICATION NUMBER: US/09/187,124A  
CURRENT FILING DATE: 1998-11-05  
EARLIER APPLICATION NUMBER: PCT/EP97/02292  
EARLIER FILING DATE: 1997-05-06  
EARLIER APPLICATION NUMBER: DE 196 18 125.9  
EARLIER FILING DATE: 1996-05-06  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 606  
TYPE: PRT  
ORGANISM: Solanum tuberosum  
US-09-187-124-2

Query Match 5.1%; Score 232.5; DB 4; Length 606;  
Best Local Similarity 20.6%; Pred. No. 8.9e-14;  
Matches 121; Conservative 87; Mismatches 165; Indels 215; Gaps 29;

296 EKYVFNKPQKRPKSLRYESHV-GMSSTEPVINTYANFRDQV---LPRIKIKYNAVQ 351  
28 EGDLLKRPQ---RDVIYEMHVRGFTNHESSETKIPGTYLVYKELDKLKGVCIE 83  
352 LMAIOESH---YVA-----SEGYHVTNFAASRPF-----GTPDDLKSL 387  
84 LMPCHFEFNELEYSYNSVLDGYKFNEMGYSTVNFSPMGRRSSAGLSNCGAINERKYL 143  
388 IDKAHELGLVLMIDYHSHASTYTLGLNFDGTDGHEHSGRHHMMWSLSLFNYGSEVLR 443  
144 VKEAKRRIEIVIMDVFNHTEGNEENGLISFRGIDNSVEFTLAPKGEFYNYSGCGNTFN 203  
444 YGSEVLEFLISNARWMLDEKKEPGEFPGDVTSMYTHHGLQVDFGNTNMEYCYATDVA 503  
204 CNNPYVRQPIYDCLRYWTEHNVDFGRD-LASTL-----TRSSSNVAVNYGNSIDGD 257  
504 AV-----VYLMNDMLHGLPEAVTIGEDVSGMPTVCIPVEDGCVGDFRILHMA 550  
258 MITGTPLTSPPLIDMISNDPL-----LSGVKLIAMWCCGL---YQGMF 301  
551 -HMAVADKWEIIOKREDNMKSGDVIHMLNRMLEKCVSYAESHDQALVGDKT----- 604  
302 PHWGIVSEW-----NGKYRDMV-----ROPKIGTDFSGAFACLGSPALYQKG 347  
605 -----AFWLMQDKMD----- 615  
348 KRPWNSINFCVADHGFVLADLVITNNKHNLANGEDNKDGENHNNSWNCGESEFASTLVK 407  
616 -----FMALDRPSTPLIDRGVALHKMIRLITMGLGEGVYINFMGNFEPHWD 665  
408 KLRKQKRNPFCL-----WVSGCV-----MIYMDGYGHTK----- 440  
666 PRGLHLPSGKFPVGNNSYDCKRRR-----DLGNSKHLRNG-MOEPDQALDHL 715  
441 -----GGNNNTY--CHDNYINFRMDKDESSDFLFGCLMTKRHECESL 485  
716 EEAVGEMTSE---HOYISRK---DERDRIYVE---RGNLVFVFN 751  
486 -GLDGFPAERLQWGHPTKPTDMSETSRVAVFLYDKVAGELYIAFN 532

RESULT 8  
US-08-961-083-80

Sequence 80, Application US/08961083  
Patent No. 6139469  
GENERAL INFORMATION:  
APPLICANT: Choi et. al.  
TITLE OF INVENTION: Streptococcus pneumoniae Antigen and Vaccines  
NUMBER OF SEQUENCES: 452  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland

Tue Aug 7 20:32:51 2001

us-09-297-703a-29.ra1

Page 6

COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/961,083  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PB340P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8512  
TELEFAX: (301) 309-8504  
INFORMATION FOR SEQ. ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 325 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-961-083-80

Query Match 5.0%; Score 226; DB 4; Length 325;  
Best Local Similarity 25.2%; Pred. No. 1.3e-13;  
Matches 79; Conservative 44; Mismatches 94; Indels 96; Gaps 14;

QY 388 IDKAHEGLVLMIDIVSHASTNTLDGLNMFDTGTHYFHSGRGHHMMWDSRLFNYSW 447  
DB 3 VEECHTHNIGIVDMVPHXHEFTIND-DALAYYDGTPTREYODHNKANHNGALNFDLGN 61  
QY 448 EVLFELLSNAWMIIDEXKDFRFDGVTSMWYTHNGLOVFT-----GNYNEFGYATDV 502  
DB 62 EVQSFLLSCIKHWIDVYHLDGIRVDASNNMLYLDYD-DAVPTPKDGNLN-YEGY---- 115  
QY 503 DAVVYMLNMGIGPREVATIGEDVSGMPTVCIPVEDGSGVDYRLHMAVADKWEII 562  
DB 116 ---YFLQRLNVIKLEPRDVMMIAESSSAIKIKGMKEIGSGFDYK----- 159  
QY 563 QKRDEKMGDIYHMLNRRWLEKCYSAE-----SHDQALYGDKTIAFWLMDKMY-- 614  
DB 160 -----MMNG-----MMNDILRFYEDDPIYRKIDENLV---TFSEYVYAKENYLL 200  
QY 615 ---DEMAIDRPSRLIDRGVALHKKRILTMGLGEGY-----L 650  
DB 201 PFSHDEVVHGKRS-----MMHKM-----WGDKYNOFAGLRMLYTOICHPEKKL 244  
QY 651 NFMGNFEGH-PEW 662  
DB 245 LFMGSEYGOFLFW 257

RESULT 9  
US-08-399-646-2  
Sequence 2, Application US/08399646  
Patent No. 5556781  
GENERAL INFORMATION:  
APPLICANT: KUBOTA, Michio  
APPLICANT: TSUSAKI, Keiji  
APPLICANT: HATTORI, Kazuko  
APPLICANT: SUGIMOTO, Toshiyuki  
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND  
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
City: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/399,646  
FILING DATE: 07-MAR-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 59834  
FILING DATE: 07-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 59840  
FILING DATE: 07-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: KUBOTA-5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ. ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 389 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-399-646-2

Query Match 4.9%; Score 224.5; DB 1; Length 519;  
Best Local Similarity 20.3%; Pred. No. 5.1e-13;  
Matches 133; Conservative 90; Mismatches 248; Indels 83; Gaps 29;

QY 216 GFNNNNPNADWYTONCEGWEIFLNNADSGPPIPHGSRVKIRMDTPSG-----N 266  
DB 8 GRFDIAPAPRAGVTLIAGG--ERYEGRPRGNGPADEGWMT--AADAPTADVNYGYLLD 63  
QY 267 KDSIPAMIKFSVOAPGELPYNGIY-----YDPREEKYVFKNPQPKRPSLRIYESHVGM 321  
DB 64 GDEIPLPDRPTRRPP-----EGVHALSRFTD--PGANRMODAGMGRELQGSYVIELHIGT 117  
QY 322 SSTPEVINTYANFRDVLPRIKKLYNNAVQMAIOESHYSYASFGYHVNIFYAASRFGTP 381  
DB 118 FTPEGLDAAAG--KLDYLAGLGDIFELLRYVNAFNGTNHWGVDGYOWFAVIEGYGSP 173  
QY 382 DDIKSLIDKAHEGLVLMIDIVSHASTNTLDGLNMFDTGTHYFHSGRGHHMMWDSRLFNYSW 447  
DB 174 AAYQRFVDAAHAAAGLGYIDVYVYNNH-----GPSNLYLPRPGTYIKIHSEGMTW 221  
QY 436 MMDSRLENTGSGWEVRLFLLSNAWMIIDEXKDFRFDGVTSMWYTHNGLOVFT----- 495  
DB 222 GDSVNLDPGSDHYROYLLDNVAMWLRDVRVGLRIDAV-----HALKDRRAVHIIEE 274  
QY 496 FGATVDVAVVVYMLNDMIGHLFFPEA---VTIGEDVSGMPTVCIPVEDGCVJ----- 545  
DB 275 FGALAD-----ALSSGGRPLTLIAESDLNRPRLYPRDVNGYSLAGQMS 319  
QY 546 --FDYRLHMAVADKWEIIQKRDEKMGDIYHMLTN-----RMLKCK----- 587  
DB 320 DDHNAHVNVNNGSETGYSDPD---SIGALAKVLRDGFHDSYSSPRGRCHGPRINFS 376  
QY 588 -----VYASHDQALYGDKTIAFWLMDKMYQFMA-----LDRPSTPLIDGVALH 634  
DB 377 AVHPALVYCSQNHQ--IGNRATGRLSQSLPYGSLAALAVLTLGTPTPL----- 427



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Db      8 GREDVIMPEAGVYTLLAGG--EKYEMGRRGNGNPADEGWT--AADAPPGADVDYGYTLTD 63
QY      267 KDSIPAMIKTSVQAPGELPNNGIY-----YDPPEEKYVFKNPQRPKRSLRIYESHYGM 321
Db      64 GDELPIDPPPTRRQP-----EGVHALSTRFD--PGAHNRWODAGWQCRHLOGSVYIELHGT 117
QY      322 SSTEPVINTVANNRDVLPRIKKIGVNAVOALAIQEHSHVSAFCGHVYTNFPAASSRGTP 381
Db      118 FTPEGLDDAAG--KDIYLAGIGIDFIELLPVAFNGTHWGWGDGYWMPVAHEGGGP 173
QY      382 DDLSLIDKAHELGLVLMDDIYHSHASTNTLDGLNMFPGTDGHYF--HSGP-----RGHH 435
Db      174 AAYQRVVDAAHGAAGLGVIODVYVNH-----GPSGNLPRGYLKKGBEWTW 221
QY      436 MMSDFENFGSMVEVLPBLLSNARWMLDEKPDGFRFGDVTSMATTHGLQVDFGTANYEY 495
Db      222 GDSVINIDGSGSHVROYLTIDNVAMMLRDYRVGGLRLAV-----HALDERAVHILTE 274
QY      496 FGATVDVAVVYIMLMDIMHGLFPEA-----VTIGEDVSGMPVCIPVEGGVG----- 545
Db      275 FGALAD-----ALSEGGRRPLTILAESLNNPRLTYRDNVNGTGLAGQWS 319
QY      546 --FDYILHAAVADKVEIILQKREDWMKGDIVHMLTN-----RWLEKC----- 587
Db      320 DDFHAHVHANNVSGETTYGYSDFD---SLGALAKVLRDGFHDGSSSFRGRGRPNFS 376
QY      588 -----VSASHQOALVGDKTIAFWLMDMDWDMA-----LDRPSPLIDRGVALH 634
Db      377 AVHPALAVVCSQNHQ--IGNRATGDRLSQSLPGSIALAAVLTLTGPFPMI----- 427
QY      635 KAIRLITMGLGEGYILNFMGNEFG-----HPWIDFPRGDLHLPSGKFPVGNYS 684
Db      428 -----FMGEYGATTPWQGFETSHPE-----PELGRATAGRIREFEERG 466
QY      685 YDKC-----RRRFDLGSK---HLR--YHGQEDQALQHLLEAYGFMISE 725
Db      467 WDPAYVPPQPEPTTSKSLDMAASAGDHARLLEYRSLTLRRSTPELAR--LGFADTA 525
QY      726 HOYSRKDERRIIVFERGNLVFNFHMTSSYSDYVGCGLKPKKVIYDSD 779
Db      526 VEF-----DDARMLRWMGVGVVYVNF-----ADRPISLDRGCT--ALLATDD 568

RESULT 11
US-08-961-240-2
? Sequence 2, Application US/08961240
? Patent No. 5830715
? GENERAL INFORMATION:
? APPLICANT: KUBOTA, Michio
? APPLICANT: TATSUKI, Keiji
? APPLICANT: HATTORI, Kazuko
? APPLICANT: SUGIMOTO, Toshiyuki
? TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
? NUMBER OF SEQUENCES: 18
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: BROWDY AND NEIMARK
? STREET: 419 Seventh Street, N.W., Suite 300
? CITY: Washington
? STATE: D.C.
? COUNTRY: USA
? ZIP: 20004
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/961,240
? FILING DATE: 30-OCT-1997
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/399,646

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Tue Aug 7 20:32:51 2001

us-09-297-703a-29.rai

Page 8

FILING DATE: 07-MAR-1995  
APPLICATION NUMBER: JP 59834  
FILING DATE: 07-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 59840  
FILING DATE: 07-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: KUBOTA-5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 589 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-961-240-2

Query Match 4.9%; Score 224.5; DB 2; Length 589;  
Best Local Similarity 20.3%; Pred. No. 5.1e-13;  
Matches 133; Conservative 90; Mismatches 248; Indels 183; Gaps 29;

216 GDFNNMNPADVYQNEGWEIPLPNNADGSPPIPHGSRVYKIMDTPSG-----N 266  
8 GRDINAPAGVYTLAAG--ERYEMGRPRGNGPADEGWMT--AADAPTGDVYGYLLD 63  
267 KDSIPAMIKESVQAPGELPYNGIY-----YDPPEEKYVFKNPQPKRKSLRIYESHVGM 321  
64 GDEIPLDPDRTRKP-----EGVHALSRFPD-PGHRWQDAGMOCRELQSGVITELHIGT 117  
322 SSTEPVINTYANFRDVLPRIKLGYNAVQMAIOESHYASFGYHVTNFYAAASRFGTP 381  
118 FTPEGTLDAAG--KLDYLAGIDFIELPLPVNAFNGTHNMKGVDGYQWFAVHVGCGP 173  
382 DDLKSLIDKAHELGLLVLMIDIVHSASTNTLDGLNFDGTDGNYF-HSGP-----RGHNW 435  
174 AAYQRFVDAHAAGLGVYIDVYVYNNH-----GPSGNYLPRYGPYLIKHEGNTW 221  
436 MMDSRLEFNYSWEVLRFLLSNARWMLDEYKDFGFRDGYTSMYTHHGLQVDFGNYNEY 495  
222 GDSVNLDPGSDHVRQYIILDNVAMMLRDYRVGLRLDAV-----HALKDRRAVHILEE 274  
496 EGYATDVDAVVYVLMIDMTHGLFPEA--VTIGEDVSGMPTVCIPVEDGCVG-----545  
275 FGALAD-----ALSSGGRPLFLIAESDLNPNRLLYPRDVGNGYLAGQWS 319  
546 --PYRLHMAVADKWEIIOKREDEKMGDIYHMLTN-----RRMLEK-----587  
320 DDFHNAHVAVSGETGYSDPD--SLGALAKVLKDFGHDGYSVSFGRHGRPINFS 376  
588 -----VSAESHDOALVGDKTIAFMIMDKYUDFMA-----LDRPSTPLIDRGVALH 634  
377 AVHRAALVYCSQNDQ--IGNRATGRLSGLPYGSIALAAVLLTGCPPTML-----427  
635 KAIRLITMGLGEGYLTFEMNGNEF-----HPEWIDFPRGDDHLBSGFVFPQNNYS 684  
428 -----FKGEFYGATTPMQFPTSHP-----PELGKATAGRIREFERRMG 466  
685 YDKC-----RRRDLGNSK--HLR-----YHGQEPDOALIONHEEYGFMTSE 725  
467 WDPAVVPDPDEPFTTSKLDMAASAGDIARLLELYRSLITLRSPPELAR-LGFDATA 525  
726 HOYSRKDERDRIIVFERGNLVYFVFNHWTSYSYDIYVGLKPGKXYIADSD 779  
526 VEF-----DDARMLRYMRGQVYVNLN-----ADRPISIDRFET-ALLATAD 568

RESULT 12

US-08-605-501-2  
Sequence 2, Application US/08605501  
Patent No. 5834287  
GENERAL INFORMATION:  
APPLICANT: KUBOTA, Michio  
APPLICANT: TSUSAKI, Keiji  
APPLICANT: HATTORI, Kazuko  
APPLICANT: SUGIMOTO, Toshiyuki  
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND  
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: BROWDY AND NEWMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/605,501  
FILING DATE: 26-FEB-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/399,646  
FILING DATE: 07-MAR-1995  
APPLICATION NUMBER: JP 59834  
FILING DATE: 07-MAR-1994  
PRIOR APPLICATION DATA: JP 59840  
APPLICATION NUMBER: JP 59840  
FILING DATE: 07-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: KUBOTA-5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 589 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-605-501-2

Query Match 4.9%; Score 224.5; DB 2; Length 589;  
Best Local Similarity 20.3%; Pred. No. 5.1e-13;  
Matches 133; Conservative 90; Mismatches 248; Indels 183; Gaps 29;

216 GDFNNMNPADVYQNEGWEIPLPNNADGSPPIPHGSRVYKIMDTPSG-----N 266  
8 GRDINAPAGVYTLAAG--ERYEMGRPRGNGPADEGWMT--AADAPTGDVYGYLLD 63  
267 KDSIPAMIKESVQAPGELPYNGIY-----YDPPEEKYVFKNPQPKRKSLRIYESHVGM 321  
64 GDEIPLDPDRTRKP-----EGVHALSRFPD-PGHRWQDAGMOCRELQSGVITELHIGT 117  
322 SSTEPVINTYANFRDVLPRIKLGYNAVQMAIOESHYASFGYHVTNFYAAASRFGTP 381  
118 FTPEGTLDAAG--KLDYLAGIDFIELPLPVNAFNGTHNMKGVDGYQWFAVHVGCGP 173  
382 DDLKSLIDKAHELGLLVLMIDIVHSASTNTLDGLNFDGTDGNYF-HSGP-----RGHNW 435  
174 AAYQRFVDAHAAGLGVYIDVYVYNNH-----GPSGNYLPRYGPYLIKHEGNTW 221  
436 MMDSRLEFNYSWEVLRFLLSNARWMLDEYKDFGFRDGYTSMYTHHGLQVDFGNYNEY 495

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Db      222 GDSVNLDPGSDHVRQYLLDNVAMWLRDVRVGLRLDAV-----HALKDERAVHILTEE 274
      496 FGATVDVAVVYLLMLNDMIGHLEPEA-----VTIGEDVSGMPTVCIPVDGCVG----- 545
      275 FGALAD-----ALSSGGRRPLLLIAESDLNRPRLYPRVNYGTGLAGQMS 319
Qy      546 --FDYRLHMAVADKWEIIOKDEDEMKMGDIYHMLTN-----RRLMEKC----- 587
      320 DGFHHAHVNVSGETGYSDFD--SLGALAKVLRDGFHHDGYSVSFRRCHGRPIINS 376
Qy      588 -----VYASHDQALVGDKTIAFWLMDKMYDPMA-----LDRPSTPLIDGVALH 634
      377 AVHAPALVVCSONHDQ--IGNRATGDRLSQSLPYGSLAAVLLTLPPTPML----- 427
Qy      635 KMIRLITMGLGEGYLNFGNENFG-----HPEWIDFPRGDLHPSGKFPVGNYS 684
      428 -----FMGEYEGATTPWQFTSHPE-----PELGKATAGRIREFERRMG 466
Qy      685 YDKC-----RRRFDLGNSK--HLR-----YHGMQEPDQAIQHLBAYGPMTSE 725
      467 WPAVAVPDPODEPFTFRSKLDMAEASAGDHARLLELYRSLTLTRSTPELAR-LGFADTA 525
Qy      726 HOYISRKDERDRIIVFERGNLVFENFHWTSYSDYRVGCLPKGKYIVLSDSD 779
      526 VEF---DDDAWMLRYWRGVQVYVLFN-----ADRPISLDRPGT-ALLATDSD 568

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## RESULT 13

US-08-399-646-12  
Sequence 12, Application US/08399646  
Patent No. 5556781

```

GENERAL INFORMATION:
APPLICANT: KUBOTA, Michio
APPLICANT: TSUSAKI, Keiji
APPLICANT: HATTORI, Kazuko
APPLICANT: SUGIMOTO, Toshiyuki
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESS: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/399,646
FILING DATE: 07-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 59834
FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 59840
FILING DATE: 07-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: KUBOTA-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 596 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-399-646-12

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Query Match 4.9%; Score 224.5; DB 1; Length 596;  
Best Local Similarity 20.3%; Pred. No. 5.2e-13;  
Matches 133; Conservative 90; Mismatches 248; Indels 183; Gaps 29;

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Qy      216 GDFNNMNPNDVMTQNEGVWEIFLPNNADSGPRIPGSRKIKIMDPPSG-----N 266
      15 GRFDIMAEAGTVLLAG--ERYEMGRPGNGPADGGMWT--AADAPGADVDDYGLLD 70
Qy      267 KDSIPAMIKFSVOAPGELPYNGIY-----YDPPEEKYVFKNPQPKRSLRIYESHVGM 321
      71 GDEIPLPDPRTTRQP-----EGVALHSTFDP-PAHNRQDAGMOGRELQSGYIELHIGT 124
Qy      322 STEPEVINTYANFRDVLPRIKLGYNAVQDMAIOEHSYASFGYHVTNFAASSRPGTP 381
      125 FTPEGTDLDAAG--KIDYLAGIGIDIELLPVNAFNGTHMGVGDGVQWFAVHEGYGFP 180
Qy      382 DDLKSLIDKAHELGLVYMDIVHSHASNTIDGLMFDGDGHF--HSGP-----RGHHW 435
      181 AAYQREYDAHAAGIGVLDVYVYVNL-----GPSGNLYPRYGPYLKHGEGNTW 228
Qy      436 MWDRLFNFGSMEVLRFLLSNARWMLDEYKPGDFRPGVTSMTYTHGLQVDFGNNEY 495
      229 GDSVNLDPGSDHVRQYLLDNVAMWLRDVRVGLRLDAV-----HALKDERAVHILTEE 281
Qy      496 FGATVDVAVVYLLMLNDMIGHLEPEA-----VTIGEDVSGMPTVCIPVEDGCVG----- 545
      282 FGALAD-----ALSSGGRRPLLLIAESDLNRPRLYPRVNYGTGLAGQMS 326
Qy      546 --FDYRLHMAVADKWEIIOKDEDEMKMGDIYHMLTN-----RRLMEKC----- 587
      327 DGFHHAHVNVSGETGYSDFD--SLGALAKVLRDGFHHDGYSVSFRRCHGRPIINS 383
Qy      588 -----VYASHDQALVGDKTIAFWLMDKMYDPMA-----LDRPSTPLIDGVALH 634
      384 AVHAPALVVCSONHDQ--IGNRATGDRLSQSLPYGSLAAVLLTLPPTPML----- 434
Qy      635 KMIRLITMGLGEGYLNFGNENFG-----HPEWIDFPRGDLHPSGKFPVGNYS 684
      435 -----FMGEYEGATTPWQFTSHPE-----PELGKATAGRIREFERRMG 473
Qy      685 YDKC-----RRRFDLGNSK--HLR-----YHGMQEPDQAIQHLBAYGPMTSE 725
      474 WPAVAVPDPODEPFTFRSKLDMAEASAGDHARLLELYRSLTLTRSTPELAR-LGFADTA 532
Qy      726 HOYISRKDERDRIIVFERGNLVFENFHWTSYSDYRVGCLPKGKYIVLSDSD 779
      533 VEF---DDDAWMLRYWRGVQVYVLFN-----ADRPISLDRPGT-ALLATDSD 575

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## RESULT 14

US-08-607-321-12  
Sequence 12, Application US/08607321  
Patent No. 5716813

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GENERAL INFORMATION:
APPLICANT: KUBOTA, Michio
APPLICANT: TSUSAKI, Keiji
APPLICANT: HATTORI, Kazuko
APPLICANT: SUGIMOTO, Toshiyuki
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESS: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA

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? ZIP: 20004
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/607,321
? FILING DATE: 26-FEB-1996
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/399,646
? FILING DATE: 07-MAR-1995
? APPLICATION NUMBER: JP 59834
? FILING DATE: 07-MAR-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: JP 59840
? FILING DATE: 07-MAR-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: BROWDY, Roger L.
? REGISTRATION NUMBER: 25,618
? REFERENCE/DOCKET NUMBER: KUBOTA-5
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 202-628-5197
? TELEFAX: 202-737-3528
? TELETEXT: 248633
? INFORMATION FOR SEQ ID NO: 12:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 596 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-607-321-12

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Query Match 4.9%; Score 224.5; DB 1; Length 596;
Best Local Similarity 20.3%; Pred. No. 5,2e-13;
Matches 133; Conservative 90; Mismatches 248; Indels 183; Gaps 29;

```

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QY 216 GDENNMNNADVYVQNECGWVEIFLPPNADGSPPIPHGSRVIRIMDTPSG-----N 266
DB 15 GRFDIMAEAGVITLLAG--ERYEMGRPRNGPDEGWT--AADAPTGAADVYGYLLD 70
QY 267 KDSIPAMIKFSVQAPGELPYNGIY-----YDPEEEKYVFNKPPQKPKSLRTIESHYGM 321
DB 71 GDEILPDPKTRKOP-----EGVHLSKTFD-PCAHNMQDAGWGRELQSGVITELHIGT 124
QY 322 STEPVINTVYVNFQDVLPRIKKLGYNAAVQMLAQIHSYVSPGYHVTNYFAASSRFQTP 381
DB 125 FTPEGTLDAAAG--KLDYLAGLIDITELLPVNAFNGTHNMGIDGVQWFAVEHGYGGR 180
QY 382 DDLKSLIDKAHELGLVLMIDIVHSHASTNTLDGLNMDGDTGXYF-HSGP-----RGHHW 435
DB 181 AAYQRFVDAHAAGAGVYIDVYVYVNL-----GPSGNLIPRYGRLKKGEGNTW 228
QY 436 KWDSELFNYGSEWYVRELLSNARWMLDEKDFGRFDGVTSMATYHGLQVDFGTNTNEY 495
DB 229 GDSVMLDPPGSDHYKQXITLDVNAWMLRBYRVGGLDAV-----HALKDERAVHILEE 281
QY 496 FGATVDVAVVYVLMILNDIMIGLPEEA-----VTIGEDVSGMPYVCIPEVDGAGV----- 545
DB 282 FGALAD-----ALSEGGRLPLTLAESDLNPRILYPRDVGYGLAGQWS 326
QY 546 --FDYRLHNAVADKWEITQKREDEMKMGDIVHMLTN-----RRMLEK----- 587
DB 327 DDFHNAVAVNVSGETTYGSPD--SIGALAKYLROGFFHDSYSSRFGCHRPINF 383
QY 588 -----VSYESHDOALVGDKTAFWLMKMDYDENA-----LDRSPFLIDRGVALH 634
DB 384 AVHRAALVYVCSNDDQ--IGNRAIGDRLSQSLLPGSLAVALVLTIGFTML----- 434
QY 635 KMRLITMGLGEGYLNMGNEFG-----HPEKIDPPRGDLHLPSKRYVPGNNYS 684

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DB 435 -----FMGEYGATTPMOFTSHPE-----PELGNATGGRINIEFERMG 473
QY 685 YDKC-----RRRFDLGNK--HLR-----YHGMQFDOALQHLERAGCFMTSE 725
DB 474 WDAVAVPDPDDETFYRSLDMAEASAGDHARLELYRSLITLRSTPELAR-JGFADTA 532
QY 726 HOYISKRDEDRRIYVERGNLVFVFNHWTSSYSYDRCGLPGKXKYLDSDD 779
DB 533 VER-----DDARWLRYMRGQVVLNF-----ADRPISLDRPT-ALLIARD 575

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RESULT 15
US-08-961-240-12
; Sequence 12, Application US/08961240
; Patent No. 5830715
; GENERAL INFORMATION:
; APPLICANT: KUBOTA, Michio
; APPLICANT: TSUSAKI, Keiji
; APPLICANT: HATTORI, Kazuko
; APPLICANT: SUGIMOTO, Toshiyuki
; TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,240
FILING DATE: 30-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,646
FILING DATE: 07-MAR-1995
APPLICATION NUMBER: JP 59834
FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 59840
FILING DATE: 07-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: KUBOTA-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELETEXT: 248633
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 596 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-961-240-12

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```

Query Match 4.9%; Score 224.5; DB 2; Length 596;
Best Local Similarity 20.3%; Pred. No. 5,2e-13;
Matches 133; Conservative 90; Mismatches 248; Indels 183; Gaps 29;

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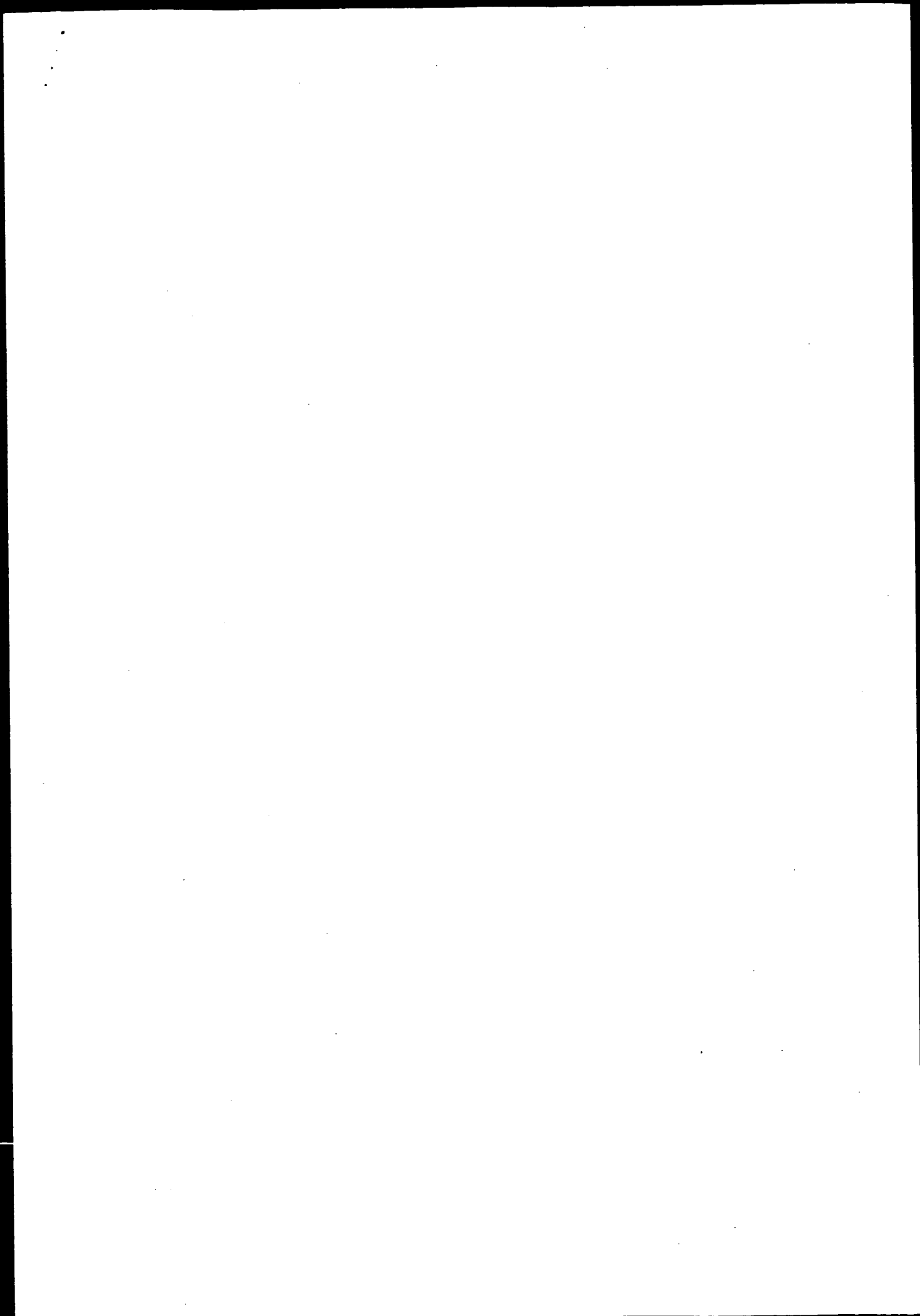
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QY 216 GDENNMNNADVYVQNECGWVEIFLPPNADGSPPIPHGSRVIRIMDTPSG-----N 266
DB 15 GRFDIMAEAGVITLLAG--ERYEMGRPRNGPDEGWT--AADAPTGAADVYGYLLD 70
QY 267 KDSIPAMIKFSVQAPGELPYNGIY-----YDPEEEKYVFNKPPQKPKSLRTIESHYGM 321

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Db 71 GDELPDPKTRROP-----BGVHALSRTFD-PGAHRWQDAGWQRELOGSVIEYELHIGT 124
QY 322 SSTEPVINTYANFRDVLPRIKKLGYNVAVOLMAIOESHYASFGYHTNFEYAASSRGTP 381
Db 125 FTPEGTIDMAAG-----KLDYLAGIDIFIELLPYNAENGTHNWGYDGVOMFAVHEGYGP 180
QY 382 DDLKSLDKAHELGLVIMDIVHSHASTNTLDGLNMFDTGDHYF-HSGP-----RGHHW 435
Db 181 AAYGRFYDAHAAGLGYODVYVNNH-----GPSGNYLPYRGPLYKHGEGNTW 228
QY 436 MMDSRLEFNYSWEYLRFLLSARWMLDEYKEDGFRFDGYISMTTHHGLQYDFTGNNEY 495
Db 229 GDSVNLGPGSDHYRQYTLIDVAMMLRDYRVDGLRIDAV-----HALKDERAVHITLEE 281
QY 496 FGATDVAVVYMLLNDMTHGLEPPEA-----VTIGEDVSGMPTVCIPVEDGVG----- 545
Db 282 FGALAD-----ALSSEGGRLVTLAESDLNPNRLYPYRDVNGYGLAGQWS 326
QY 546 --FYRLHMAVADKWEVLIQKREDEMKMGDI VMLTN-----RRMLEKC----- 587
Db 327 DDEFHAAVHVNVSGETTGYSDFD---SIGALAKVLRDGFPHDGSYSSFRGRCHGRPINFS 383
QY 588 -----VSYAESHDOALVGDKTIAFWLMDKMDWDEMA-----LDRPSTPLIDRGVALH 634
Db 384 AVHRAALVVSQNHDO--IGNRATGDRLSQSLPFGSLALAAVLTGPFPTPML----- 434
QY 635 KMIRLITMGLGEGYLNFNGNEFG-----HPEWIDPFRGDLHLPSGKFVPNGNYS 684
Db 435 -----FMGEYEGATTPMQFTSHPE-----PELGKATAGRIREFBRMG 473
QY 685 YDKC-----RRRFDLGNSK---HLR-----YHGMOEFDQAIQHLLEAYGEMTSE 725
Db 474 WDPAYVPPDPODPETFRSKLDMAEASAGDHARLLELYRSLITLRSTPELAR-LGFAADTA 532
QY 726 HOYISRKDEDRRIIVEFNGNLVFNPNHMTSSYSDYRVGCLKPKXKIYVDSDD 779
Db 533 VEF-----DDARWLRYWRGSGVQVYVNF-----ADRPISLDPRGT-ALLIATDD 575
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Search completed: August 7, 2001, 11:19:14  
Job time: 291 sec



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OY 4 YTISGIFFPAP-LTCSQSOTGFHGRRTSSCLSF--PNKEAFSARFVSCGSHSEDSNV 60
      -|-----|-----|-----|-----|-----|-----|-----|-----|
Db 3 YTISGIFFPVLPILHST---LQCRBRASSHSFPLKNNSSFSFTSLIYAFSHDSETKSS 59
      -|-----|-----|-----|-----|-----|-----|-----|-----|
OY 61 MTAASKRVLPDGRICEYSSSTQDLEAPGVSEESQVLTDESILMD-----10
      :|-----|-----|-----|-----|-----|-----|-----|-----|
Db 60 TIESDKVLLPEODNSVSLAQLENDPITSEDAQ---NLEDLTMDGKNYNIDSTSSY 11
      -|-----|-----|-----|-----|-----|-----|-----|-----|
OY 108 KIYADE-----VAKESVPRRETV-SIRKIG-SKRSRTPPGRCQRITYIDPSLT 15
      :|-----|-----|-----|-----|-----|-----|-----|-----|
Db 117 REVGEDEKGSYSSSLVDVNTDQAKKTSVSHDKKVKYKDKRKIIPPGTQOKIYEIDPLQ 17
      :|-----|-----|-----|-----|-----|-----|-----|-----|
OY 155 GFROHLDYRYSQKRLREBIDKIESLSLAFSRGKRGFSESTGTYREMAPGATMAL 21
      -|-----|-----|-----|-----|-----|-----|-----|-----|
Db 177 AHROHLDYFRGQYKRIREBIDKIEGGLDAFSGYKENGKFLRSMTGITYREMAPGAKSAL 23
      -|-----|-----|-----|-----|-----|-----|-----|-----|
OY 215 ISGFNNMNNNAVVMONCGWEIIFLPPNADGSPPIPHGSRVKTIRMDTPSGAKSDIPAMI 27
      :|-----|-----|-----|-----|-----|-----|-----|-----|
Db 237 VGDFNNMNNNAVVMKDAFGWEIIFLPPNADGSPPIPHGSRVKTIRMDTPSGIKSDIPAMI 29
      -|-----|-----|-----|-----|-----|-----|-----|-----|
OY 275 KFSVQAPGELPYNGIYDPPPEBEKYVFNKQPKRPSLIRYESHVMGMSSTEPVINTYANF 33
      -|-----|-----|-----|-----|-----|-----|-----|-----|
Db 297 KFSVQAPGELPYNGIYDPPPEBEKYVFNKQPKRPSLIRYESHVMGMSSTEPVINTYANF 35
      -|-----|-----|-----|-----|-----|-----|-----|-----|
OY 335 RDOVLPRIKKLGNNVQMLAQEHSYASTSGYHVNIFYAASRFGTDDLSLIDKAHEL 39
      -|-----|-----|-----|-----|-----|-----|-----|-----|

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Db 357 RDDVLPRIKIKLGYNVQJMAIOEHSTYASFGYHVNFPAPSSRFQTPEDLSIDRAHEL 416  
 QY 395 GLLVYMDIVHSHASTNTDGLNMFPGDGHFHSQPRGHMMMDRLFNYSWEVLRFL 454  
 Db 417 GLLVYMDIVHSHASTNTDGLNMFPGDGHFHSQPRGHMMMDRLFNYSWEVLRFL 476  
 QY 455 SNARKWLDKXGDEKDEPGYTSMTYTHGLQVDFGTGNNEFYGVATDYDAYVYLLMLNDM 514  
 Db 477 SNARKWLDKXGDEKDEPGYTSMTYTHGLQVDFGTGNNEFYGVATDYDAYVYLLMLNDM 536  
 QY 515 INGLEPEAVTIGEDVSGMPTVCIPEDDGCGPDYRLHMAVADKWEIIOKDEDMKMDI 574  
 Db 537 INGLEPEAVTIGEDVSGMPTVCIPEDDGCGPDYRLHMAVADKWEIIOKDEDMKMDI 596  
 QY 575 VMLTNRMWLEKCVSYAESHDQALVGDKTIAFWLMDKMDYDMALDRSTPLIDGVALH 634  
 Db 597 VMLTNRMWLEKCVSYAESHDQALVGDKTIAFWLMDKMDYDMALDRSTPLIDGVALH 656  
 QY 635 KMIRLITMGLGEGYLNFMGNFEGHPEWIDPRGDLHPGSKFVPQNNYSDYCKRRRDL 694  
 Db 657 KMIRLITMGLGEGYLNFMGNFEGHPEWIDPRGDLHPGSKFVPQNNYSDYCKRRRDL 716  
 QY 695 GNSKHLYRGHMOEFDOAIOHLEAAGFMTSEHQYISRKDERRIIVFERGNLVFVFNHFW 754  
 Db 717 GADADLYRGHMOEFDOAIOHLEAAGFMTSEHQYISRKDERRIIVFERGNLVFVFNHFW 776  
 QY 755 TSQSYRYRGCKLPKRYKIVLDSDDPLFCGFGRLSHDAHFSEFGYNDNRPSFMYVTPC 814  
 Db 777 TNSYSDYRYRGCKLPKRYKIVLDSDDPLFCGFGRLSHDAHFSEFGYNDNRPSFMYVTPC 836  
 QY 815 RTAVVYALVEDEYENE 830  
 Db 837 RTAVVYALVEDEYENE 851

## RESULT 2

1,4-alpha-glucan branching enzyme (EC 2.4.1.18) isoform SBE2.2 precursor - Arabidopsis thaliana  
 N:Alternate names: starch branching enzyme 2.2  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C>Date: 22-Nov-1996 #sequence\_revision 22-Nov-1996 #text\_change 18-Jun-1999  
 C:Accession: S65046  
 R:Fishar, D.K.; Gao, M.; Kim, K.N.; Boyer, C.D.; Gultman, M.J.  
 Plant Mol. Biol. 30, 97-108, 1996  
 A:Title: Two closely related cDNAs encoding starch branching enzyme from Arabidopsis thaliana  
 A:Reference number: S65045; M01D:96197401  
 A:Accession: S65046  
 A:Molecule type: mRNA  
 A:Residues: 1-800 <PI>  
 A:Cross-references: EMBL:U022428; NID:9726489; PIDN:AA03100.1; PID:9726490  
 A:Note: only a part of the coding sequence is given  
 C:Genetics:  
 A:Genome: nuclear  
 C:Function:  
 A:Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha-D-galactose  
 A:Pathway: glycogen/starch biosynthesis  
 A:Note: final step in biosynthesis of glycogen or amylopectin  
 C:Superfamily: 1,4-alpha-glucan branching enzyme  
 C:Keywords: chloroplast; glycosyltransferase; glycosyltransferase; hexosyltransferase  
 F:1-40/Domain: trans peptide (chloroplast) #status predicted <TM>  
 F:41-800/Product: 1,4-alpha-glucan branching enzyme isoform SBE2.2 #status predicted <MF>

Query Match 74.5% Score 3384.5; DB 2: Length 800;  
 Best Local Similarity 75.5%; Pred No 2.3e-237;  
 Matches 619; Conservative 80; Mismatches 86; Indels 35; Gaps 8;  
 QY 12 PCADPCYSQSTGFHGYRTSSCLSPNKE-AFSRVSGSGSSSSNNWYATSKRVLP 70  
 Db 11 PSRPL---NGFNA---GNSLTFEFKRLKPLIFAGKSAFSDSSQAISSEKVL- 62  
 QY 71 DGRICVSSSTDLQLEAPCTVSEE---SQVLTDESILMDKIVEDEYENKESVYRETYS 126

Db 63 -----VPDNIDDPGFSOLF-DLESQIME---YTEAVTREDQTIN---V 100  
 QY 127 IRKIGKPRSIIPPPGRGQRIYDIDPSLTGFRQHLDRYQYKRLPEIDKYGSLDAPSR 186  
 Db 101 VKERGVPRIYPPPGGOKKLYIEDPMLIRYNNHLDRIYQYKRLPEIDKYGSLDAPSR 160  
 QY 187 GYKRGFSRSEGTITTYREMAPGATMAALLIDENNNMPNADVMTQNECGWELFLPNADG 246  
 Db 161 GYKRGFSRSEGTITTYREMAPGATMAALLIDENNNMPNADVMTQNECGWELFLPNADG 220  
 QY 247 SPPPIHRSRKIRMDPFSNKSIPAWIKFSVQAPGELPYNGIYDPPEEKYVZNPDP 306  
 Db 221 SPALPHGSRAKIRMDPFSNKSIPAWIKFSVQAPGELPYNGIYDPPEEKYVZNPDP 280  
 QY 307 KRPKSLRTIYESHVQMSSTPEVINTYANFRDVLPRIKIKLGYNVQJMAIOEHSTYASFGY 366  
 Db 281 KRPKSLRTIYEAHVQMSSTPEVINTYANFRDVLPRIKIKLGYNVQJMAIOEHSTYASFGY 340  
 QY 367 HTNFEVASSRFPDPLKSLIDKAEHLGLVMDIVHSHASTNTDGLNMFPGDGHFHSQ 426  
 Db 341 HTNFEVASSRFPDPLKSLIDKAEHLGLVMDIVHSHASTNTDGLNMFPGDGHFHSQ 400  
 QY 427 HSGRGHMMMDRLFNYSWEVLRFLSNARKWLDKXGDEKDEPGYTSMTYTHGLQVDFGTGN 486  
 Db 401 HSGRGHMMMDRLFNYSWEVLRFLSNARKWLDKXGDEKDEPGYTSMTYTHGLQVDFGTGN 460  
 QY 487 DFTGNNEFYGVATDYDAYVYLLMLNDMIDKMDYDMALDRSTPLIDGVALH 546  
 Db 461 DFTGNNEFYGVATDYDAYVYLLMLNDMIDKMDYDMALDRSTPLIDGVALH 520  
 QY 547 DYRLHMAVADKWEIIOKDEDMKMDIYMLTNRMWLEKCVSYAESHDQALVGDKTIAFW 606  
 Db 521 DYRLHMAVADKWEIIOKDEDMKMDIYMLTNRMWLEKCVSYAESHDQALVGDKTIAFW 580  
 QY 607 WLMKDMDYDMALDRSTPLIDGVALH 666  
 Db 581 WLMKDMDYDMALDRSTPLIDGVALH 640  
 QY 667 RGDLTLPSGKRVPGNNYSYDKCRRRFDIGNSKHLRYHMOEFDOAIOHLEAAGFMTSEHQ 726  
 Db 641 RGDLTLPSGKRVPGNNYSYDKCRRRFDIGNSKHLRYHMOEFDOAIOHLEAAGFMTSEHQ 700  
 QY 727 QYISRKDERRIIVFERGNLVFVFNHFWTSSYSDYRVGCLKPGKRYKIVLDSDDPLFCGFG 786  
 Db 701 QYISRKDERRIIVFERGNLVFVFNHFWTSSYSDYRVGCLKPGKRYKIVLDSDDPLFCGFG 760  
 QY 787 RLSHDAHFSEFGYNDNRPSFMYVTPC 826  
 Db 761 RLSHDAHFSEFGYNDNRPSFMYVTPC 800

## RESULT 3

1,4-alpha-glucan branching enzyme protein isoform SBE2.2 precursor - Arabidopsis thaliana  
 N:Alternate names: protein F17C15.70  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C>Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jun-2000  
 C:Accession: T48392  
 R:Bevan, M.; Poll, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.  
 submitted to the Protein Sequence Database, March 2000  
 A:Reference number: T48392  
 A:Accession: T48392  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-805 <BEV>  
 A:Cross-references: EMBL:AL162506  
 A:Experimental source: cultivar Columbia; BAC clone F17C15  
 C:Genetics:  
 A:Map position: 5  
 A:Insertions: 42/1; 81/3; 142/2; 175/2; 189/3; 209/3; 236/3; 275/3; 303/3; 344/2; 384/2;  
 A:Note: F17C15.70  
 C:Superfamily: 1,4-alpha-glucan branching enzyme







Qy	346	GYMNVOLMAIOEHSYVASFEYHVNINFEYAAASRFPPDDKSLIDKABHGLGLVIMDIYHS	405
Db	356	GTNAVOIIMAIODEHATYASFGYHVNINFEAPSSRFETPPDKSLIDKABHGLGLVIMDIYHS	415
Qy	406	HASTNTLDGLMFDGTDGHIYHSGPRGHMMWDSRLFNFGSWEYLRLFLLSNARWMLDEYK	465
Db	416	HASKNTLDGLMFDGTDGQYFHSGSRGYHMMWDRFLFNFGSWEYLRLFLLSNARWMLDEYK	475
Qy	466	FDDGFPQCVTSMATYHNGLOVDFNGNVEYFGYATDVAVYUMLNLMINGLREPEAVTI	525
Db	476	FDDGFPDQVSMATYHNGLOVDFNGNVEYFGYSTDVAVYUMLNLMINGLREPEAVY	535
Qy	526	GEDVSGMFTVCIPIVEDGSGVGFEDYRLHMAVADRWELLQKREDBKMGDIIVMLNTRWLE	585
Db	536	GEDVSGMFAFCVPYVEDGSGVGFEDYRLHMAVADKWIELLRKREDBQVGDITPTLNRBRGE	595
Qy	586	KCVASIAEHDQALVGDKTIATFWIMDKOMYDEMALDRSTPLIDGVALHKKIIRLITWIG	645
Db	596	KCVYAASHDQALVGDKTIATFWIMDKOMYDEMAVDRQATPRVDRKIALHKKIRLITWIG	655
Qy	646	GEGYLNFGNFGHGFHEWIDFPRGDIHLPSGKFVPVONNYSYDKCRRRPDLGNSKHLRYGM	705
Db	656	GEGYLNFGNFGHGFHEWIDFPRDGHLPDRGVYIAGNNSYDKSRRRFPDLGAEYLRYHGL	715
Qy	706	QEPFOAIQHLBEAVGFMTSEHOYISRKDEBRDIYFENGNLVYFVNFHWISSYSYRGC	765
Db	716	QEPFADMONLEETGEFMTSEHOYISPKDEGRVYIYFERGNLLFNFNHWISSYSYRIGC	775
Qy	766	LKPGKXKIVLSDSDPDLFGFGFRLSHDAEHFSFEGYDNRPRSFWYITTCRATVAVYALVD	825
Db	776	SVPGKXKIVLSDSDNLSLFGGFNRLDSDASEFTSDGRHDDRCPSEFVYACRATVAVYAVDD	835
Qy	826	EVENE---LEPY 834	
Db	836	DDDDRSSILVPI 847	

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RESULT 7
T02041
1,4-alpha-glucan branching enzyme (EC 2.4.1.18) IIA - maize (fragment)
N/Alternate names: starch branching enzyme IIA
C/Species: Zea mays (maize)
C/Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 18-Jun-1999
C/Accession: T02041
R/Gao, M.; Fisher, D.K.; Kim, K.N.; Shannon, J.C.; Gultman, M.J.
Plant Physiol. 114, 65-76, 1997
A/TITLE: Independent genetic control of maize starch-branching enzymes IIA and IIB. ISOI
A/Reference number: Z14509; MUID:97303618
A/Accession: T02041
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1 814 <GAO>
A/Cross-references: EMBL:U065948; NID:q2340107; PIDN:AAB67316.1; PID:q2340108
A/Experimental source: strain B73
C/Genetics:
A/Gene: Sbe2a
C/Function:
A/Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha-D-
A/Pathway: glycogen/starch biosynthesis
C/Superfamily: 1,4-alpha-glucan branching enzyme
C/Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

Query Match 71.8%; Score 3261.5; DB 2; Length 814;
Best Local Similarity 74.0%; Pred. No. 2e-228;
Matches 604; Conservative 70; Mismatches 109; Indels 33; Gaps 5;

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QY      36  ENFKAFSRNRS-----GKSHEDSSNWTATSKRY-----LPGRICYSST- 81
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      7  FRKKAFTSYLSCAGAPKVLPGGSDDLLLSAEPVDTQPELQIPEELTVEKTS 66
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      82  DDLKAPGYSESOVLTVDESIMDKI-----VEDEVKNSVPMRTYSIRKIGS 132
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Db	67	SPQTSAVAAASSGVEAEERPELSEVIGVGGTGKIDGAGIKAKAPLVE-----E	118
QY	133	KPRSTIPPGRGORIYDIDPSLTGFRÖHLIDYRISOYKRLREEDIKTEGSLDAFSNGYEKFG	192
Db	119	KPRVTPPPGDGORIYEIDPMLGEGRGHIDYRSEYKRLRAIDÖEGDLDAFSNGYEKLG	178
QY	193	FSRSTGIGTTEEMAPGATWALLDIGNMNMNADYVMOÖEGGWEIFLPNNAÖDSPRLPH	252
Db	179	FTRSÄGILTYEEMAPGATSAALVGDENNMNADMAÖNNEGVWEIFLPNNAÖDSPRLPH	238
QY	253	GSRYKIRMDTFSGNKDSIPAMIKFSVQAPGELPYNGIYDPEEKEKYFKNPPÖKRPKSL	312
Db	239	GSRYKIRMDTFSGVKXDSIPAMIKFSVQAPGELPYNGIYDPEEKEKYFKNPPÖKRPKSL	298
QY	313	RIYESHVMSSTPEYINTYANFRDÖVLPRIKLGYNALVQALÖEHSYYASFGYHVTNFY	372
Db	299	RIYESHVMSSTPEYINTYANFRDÖVLPRIKLGYNALVQALÖEHSYYASFGYHVTNFY	358
QY	373	LAASSRFGTIPDDKLSLIDKAHELGLLYLMDIYHSHASTYTDIGLNNFDÖTÖDHHYHSGPRG	432
Db	359	LAASSRFGTIPDDKLSLIDKAHELGLLYLMDIYHSHASTYTDIGLNNFDÖTÖDHHYHSGPRG	418
QY	433	HHMMMDSLFVNGSMEVLRFLTLSNARWMLDEYKRFPGFRFDGVTSMATYHHHGLÖYDTGNY	492
Db	419	HHMMMDSLFVNGSMEVLRFLTLSNARWMLDEYKRFPGFRFDGVTSMATYHHHGLÖYDTGNY	478
QY	493	NEYEGYARDVAVVYLMILMDIMHGLFPEAVYITGEDVSGMPTVCIPVEDGGVGEDPYRLHM	552
Db	479	GEYFEGFADVDVAVVYLMILVNDLIRGLPEAVSIGEDVSGMPTVCIPYODGGGGEFDPYRLHM	538
QY	553	AYADKRWELIOKRDÖDKMKGDVYHMLITNRMLTEKCVSAEHSÖDQALVÖDKTIAFELMKD	612
Db	539	AYPDWMIELKÖSDYEWEGDVIHFLITNRMLTEKCVYTESHSÖDQALVÖDKTIAFELMKD	598
QY	613	MYDEFAALRPSTPLIDRGVALHKMIRLITMGIGGEGYINFMÖGNEGHEBMDIPFRGDLHL	672
Db	599	MYDEFAALRPSTPLIDRGVALHKMIRLITMGIGGEGYINFMÖGNEGHEBMDIPFRGDPÖSL	658
QY	673	PSGKFEVPGNNNTSYDKCRRRFDLGNKSHLRHGMOBFDQALÖHLEBAYFPMSEHOYISRK	732
Db	659	PNGSVIYPGNNNSFDCKRRRFDLGDADYLYRRGMÖBFDQALÖHLEBAYFPMSEHOYISRK	718
QY	733	DERDRIIYFERGNLVFVNFHWTSYSDYRVGCLRPKTKIYLDSDDDPLFGFGFGLSHDA	792
Db	719	HEEDVLIIFERGDILFVNFHWSNSYFYRVGCFKPKTKIYLDSDDGLFGFGFRLHDA	778
QY	793	EHFSFEGWYDNRBSFMVYTPCÖRTAVVYAL--VEDE	826
Db	779	EFTIADWPHDNRPCFSVYAPBRTAVYTPACAGADE	814

RESULT 8  
T06574  
probable 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) II precursor - wheat  
C:Species: Triticum aestivum (common wheat)  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 20-Jun-2000  
C:Accession: T06574  
R:Chibbar, R.N.  
submitted to the EMBL Data Library, August 1997  
A:Reference number: Z15769  
A:Accession: T06574  
A:Status: translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-823 <CHI>  
A:Cross-References: EMBL:Y11282; PIDN:CAAT2154.1  
A:Experimental source: cv. Fielder; kernels 12 days post anthesis  
C:Genetics:  
A:Gene: sbc2  
C:Function:  
A:Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha  
A:Pathway: glycogen/starch biosynthesis  
C:Superfamily: 1,4-alpha-glucan branching enzyme  
C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

F:1-54/Domain: transit peptide (amyloplast) #status predicted <NTP>  
F:55-823/Product: 1,4-alpha-glucan branching enzyme II #status predicted <MAT>

Query Match 71.6%; Score 3254.5; DB 2; Length 823;  
Best Local Similarity 74.9%; Pred. No. 6,5e-228;  
Matches 590; Conservative 84; Mismatches 89; Indels 25; Gaps 6;

OY 54 ESDSNVAVTAS-----KRVLPDGRIECYSSSTDLAPGVSSESVLTVESLMD--- 106  
Db 44 KSDSSRAVLSSRAAPKGLVFDG-----ESDLSAPAQ-PEELQIPEDIEETAEVNM 95  
OY 107 -----DKIVEEVNK-----ESYPMETYSIRK-IGSPRSRIPPGRQRIYDIDPSLTGF 156  
Db 96 TGTGAERLESSEPTGIVETITDGTGKGVKELVGEKPRVYKPGDGOKTIEIDPTLKDF 155  
OY 157 RQHLDIRYSQYKRLREIDIKESGLAPSRGKYEKGFSESTGITYREMAPGATMAALIG 216  
Db 156 RSHLDYRSEYRIRRAIDQHEGGLAFSRGKELGFTRSAEGITTYREMAPGASHALVG 215  
OY 217 DENNMNPADVMTONECGVWEIFLPNNADSPPIPHGSRYKIRMDTPSGNKDISIPAWIKF 276  
Db 216 DENNMNPADVMTONECGVWEIFLPNNADSPPIPHGSRYKIRMDTPSGYKDISISAWIKF 275  
OY 277 SVQAPGELPYNGIYDPEPEEKYVFNKPOKPKSLRTYESHVGMSSTPEVINTYANFRD 336  
Db 276 SVQAPGELPYNGIYDPEPEEKYVFNKPOKPKSLRTYESHVGMSSTPEVINTYANFRD 335  
OY 337 DVLPRIKLGNVAVOLMAIOEHSYASFGYHVTNFAASRFGPDPLKSLIDKAHELGL 396  
Db 336 EVLPRIKRLGNVAVOLMAIOEHSYASFGYHVTNFAASRFGPDPLKSLIDKAHELGL 395  
OY 397 LVLMDIYHSHASTWTLDGLMFGDTGCHYFSGRHHMMWDSRLPYGSGWEYLRLTSLN 456  
Db 396 LVLMDIYHSHSNNITLDGLNGFDTGCHYFSGRHHMMWDSRLPYGSGWEYLRLTSLN 455  
OY 457 ARWLDYKKGDFRFGDVTSMYTHHGLQVDFTCNNEYGYATDVAVYLLMLNDMTH 516  
Db 456 ARWLDYKKGDFRFGDVTSMYTHHGLQVDFTCNNEYGYATDVAVYLLMLNDMTH 515  
OY 517 GLPFAVITIGEDVSGMPTVCIPVEDGVGFQYRLHMAVADKWEITIOKREDDMKGDIVH 576  
Db 516 GLPFAVITIGEDVSGMPTVCIPVEDGVGFQYRLHMAVADKWEITIOKREDDMKGDIVH 575  
OY 577 MLNNRRLKCYVYAESHDQALVGDKTIAFWLMDKMDYDMALDRSTPLIDGVALHKK 636  
Db 576 MLNNRRLKCYVYAESHDQALVGDKTIAFWLMDKMDYDMALDRSTPLIDGVALHKK 635  
OY 637 IRLTMDLGEGLYLFNMGNEFGHPREWDIPRGLDHLPSGKFPVGNNSYKCRRRRDLGN 696  
Db 636 IRLTMDLGEGLYLFNMGNEFGHPREWDIPRGLDHLPSGKFPVGNNSYKCRRRRDLGN 695  
OY 697 SKHLRYSGMQEFDOAIQHEAYGFMTSEHQYISRKDERIRIIVFERGNLVFENFHMVS 756  
Db 696 ADFRYSGMQEFDOAMQHEAYGFMTSEHQYISRKDERIRIIVFERGNLVFENFHMVS 755  
OY 757 SYSDRYGCLKPGKRYKVLSDPPLFGGFGRLSHDAEHFSEEGMYNRRPSEWVYPPORT 816  
Db 756 SFEDRYGCLKPGKRYKVLSDPPLFGGFGRLSHDAEHFSEEGMYNRRPSEWVYPPORT 815  
OY 817 AYYVALVE 824  
Db 816 AYYVALTE 823

RESULT 9  
T06797  
Probable 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) - wheat  
N:Alternate names: 1,4-alpha-D-glucan 6-alpha-D-(1,4)-alpha-D-glucanotransferase  
C:Species: Triticum aestivum (common wheat)  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 18-Jun-1999  
C:Accession: T06797  
R:Kroeger, C.; Loerz, H.; Luetticke, S.

submitted to the EMBL Data Library, August 1996  
A:Reference number: Z15822  
A:Accession: T06797  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-729 <KRO>  
A:Cross-references: EMBL:U66376; NID:g1620661; PIDN:AA017086.1; PID:g1620662  
A:Experimental source: cv. Florida; kernels Z1 DAP  
A:Function:  
A:Description: converts amylose into amylopectin; catalyzes the formation of 1,6-gluc  
A:Pathway: starch and sucrose metabolism  
C:Superfamily: 1,4-alpha-glucan branching enzyme  
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 70.6%; Score 3209; DB 2; Length 729;  
Best Local Similarity 78.0%; Pred. No. 1.1e-224;  
Matches 575; Conservative 75; Mismatches 77; Indels 10; Gaps 3;

OY 88 GTVSESVLTVESLMDKIDVEEVNKESEYPMETYSIRKIGSKPSRIPFGGRQRIY 147  
Db 3 GGTAEKIQSEPTGIV--ETITGVTK--GVKELV----VGKPRVYKPGDGQKRY 52  
OY 148 DIDPSLTGFRHLDYRYSQYKRLREIDIKESGLAPSRGKYEKGFSESTGITYREMAP 207  
Db 53 EIDPTLKDFRSHLDYRYSQYKRLREIDIKESGLAPSRGKYEKGFSESTGITYREMAP 112  
OY 208 GATMAALIGDENNMNPADVMTONECGVWEIFLPNNADSPPIPHGSRYKIRMDTPSGNK 267  
Db 113 GAHSALVDEDENNMNPADVMTONECGVWEIFLPNNADSPPIPHGSRYKIRMDTPSGNK 172  
OY 268 DSIPAWIKSVQAPGELPYNGIYDPEPEEKYVFNKPOKPKSLRTYESHVGMSSTPEV 327  
Db 173 DSISAWIKSVQAPGELPYNGIYDPEPEEKYVFNKPOKPKSLRTYESHVGMSSTPEV 232  
OY 328 INTYANFRDVLPRIKLGNVAVOLMAIOEHSYASFGYHVTNFAASRFGPDPLKSL 387  
Db 233 INSYANFRDVLPRIKLGNVAVOLMAIOEHSYASFGYHVTNFAASRFGPDPLKSL 292  
OY 388 IDKAHELGLVLMNDIYHSHASTNTLDGLMFGDTGCHYFSGRHHMMWDSRLPYGSGW 447  
Db 293 IDRAHELGLVLMNDIYHSHSNNITLDGLNGFDTGCHYFSGRHHMMWDSRLPYGSGW 352  
OY 448 EVLPRLSNARWMLDEYKFGDFRFGDVTSMYTHHGLQVDFTCNNEYGYATDVAVY 507  
Db 353 EVLPRLSNARWMLDEYKFGDFRFGDVTSMYTHHGLQVDFTCNNEYGYATDVAVY 412  
OY 508 LMLNDMTHGLEPFAVITIGEDVSGMPTVCIPVEDGVGFQYRLHMAVADKWEITIOKRE 567  
Db 413 LMLVNDLTHGLTPDAVITIGEDVSGMPTVCIPVEDGVGFQYRLHMAVADKWEITIOKRE 472  
OY 568 DKRMGDIVHMLNNRRLKCYVYAESHDQALVGDKTIAFWLMDKMDYDMALDRSTPLI 627  
Db 473 SKMKMDIVHMLNNRRLKCYVYAESHDQALVGDKTIAFWLMDKMDYDMALDRSTPLI 532  
OY 628 DRGVALHKKMIRLTITMGCLGEGYLFNMGNEFGHPREWDIPRGLDHLPSGKFPVGN 687  
Db 533 DRGVALHKKMIRLTITMGCLGEGYLFNMGNEFGHPREWDIPRGLDHLPSGKFPVGN 592  
OY 688 CRRRDLGNKSLKRYHNGQEFDOAIQHEAYGFMTSEHQYISRKDERIRIIVFERGNLV 747  
Db 593 CRRRDLGNKSLKRYHNGQEFDOAMQHEAYGFMTSEHQYISRKDERIRIIVFERGNLV 652  
OY 748 FVFNHMTSSYSDYRVGCLKPGKRYKVLSDPPLFGGFGRLSHDAEHFSEEGW/DNRRS 807  
Db 653 FVFNHMTSSYSDYRVGCLKPGKRYKVLSDPPLFGGFGRLSHDAEHFSEEGW/DNRRS 712  
OY 808 FVFNHMTSSYSDYRVGCLKPGKRYKVLSDPPLFGGFGRLSHDAEHFSEEGW/DNRRS 824  
Db 713 FVFNHMTSSYSDYRVGCLKPGKRYKVLSDPPLFGGFGRLSHDAEHFSEEGW/DNRRS 729

RESULT 10

A48537  
 starch branching enzyme isoform RBE3 - rice  
 C:Species: Oryza sativa (rice)  
 C>Date: 16-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 20-Jun-2000  
 C:Accession: A48537  
 R:Minzo, K.; Kawasati, T.; Shima, H.; Satoh, H.; Kobayashi, E.; Okumura, S.; Arai, Y.  
 J. Biol. Chem. 268, 19084-19091, 1993  
 A:Title: Alteration of the structural properties of starch components by the lack of an  
 A:Reference number: A48537; MUID:93366833  
 A:Accession: A48537  
 A:Status: preliminary  
 A:Molecule type: mRNA; protein  
 A:Residues: 1-825 <MTZ>  
 A:Cross-references: GB:DL6201; NID:q4336051; PIDN:BA03738.1; PID:q4336052  
 A:Experimental source: cv. Kimmaze  
 A>Note: sequence extracted from NCBI backbone (NCBI:136747, NCBI:136748)  
 C:Superfamily: 1.4-alpha-glucan branching enzyme

Query Match Best Local Similarity 70.08; Score 3180; DB 2; Length 825;  
 Matches 586; Conservative 87; Mismatches 116; Indels 44; Gaps 7;  
 9 IRPCAPLCKSQSTGFHGRRTSSCLSFNFKAFRRVFGSKSHSDSNWVYAS--- 65  
 20 VRFPV-----PAGASWRAAALPT--SRLLSGRRPFAVVGSGGGAVAVRAGAS 70  
 66 -KRVLPDGRLE--CYSSSTQDLEAPGVSE-----ESQVLTVESLIMDKIVE 111  
 71 GEVMIPEGESGMPVYASGSDILQPLADDELSTVEGAVEIESGASDVEGV---KRV 126  
 112 DEVKESVPRREYISIKKSKRSRIPPRGGRITDIDPSLTGFQHLIDYRSQYKRLR 171  
 127 EELAAE-----OKPRVVPPTGDKIFQMDSMNGYXYHLEYRYSLEVRRLR 172  
 172 EELDKYGSIDAEASRGYKRFGRSEGTITRYREMAPATGAALIGFNNWNNADVMON 231  
 173 SDIDQEGLETFRSGYKRFGRSEGTITRYREMAPATGAALIGFNNWNNADVMON 232  
 232 ECGWELFELPNNDGSPPTPHGSRVRIKMDTPSGNKDSIPAMIKFSVQAPGLPYNGIY 291  
 233 EFGWELFELPNNDGSSPTPHGSRVRIKMDTPSGNKDSIPAMIKFSVQAPGLPYNGIY 292  
 292 DPEEEKYVFNKQPKRPSLRITYESHVGMSSTPEYINTYANFRDYLPRIKKLGYNVQ 351  
 293 DPEEEKYVFNKQPKRPSLRITYESHVGMSSTPEYINTYANFRDYLPRIKKLGYNVQ 352  
 352 LMAIOEHSTYASFGYVNTFYAASSRFGTPDDLSLIDKAHGLGLVLMIVYHSHASTNT 411  
 353 LMAIOEHSTYASFGYVNTFYAASSRFGTPDDLSLIDKAHGLGLVLMIVYHSHASTNT 412  
 412 LDGLNMFDDGTHYFHSRGHMMWDSRLFYNGSWELRFLLSNARWMLDEYKDFGRF 471  
 413 LDGLNMFDDGTHYFHSRGHMMWDSRLFYNGSWELRFLLSNARWMLDEYKDFGRF 472  
 472 DGVTSMTYTHHGLQVDFNTGNYEFGYATDVDAVYVLMILNDMIGLPEPEAVTTGDEDSG 531  
 473 DGVTSMTYTHHGLQVDFNTGNYEFGYATDVDAVYVLMILNDMIGLPEPEAVTTGDEDSG 532  
 532 MPVYCVIPVEDGCVGRDYLHMAVAADKWEIIOKRDENKMDIYHMLTNRMLEKCVSYA 591  
 533 MPVYCVIPVEDGCVGRDYLHMAVAADKWEIIOKRDENKMDIYHMLTNRMLEKCVSYA 592  
 592 ESHDQALVADKTIAMVMDKMDYDPMALDRPSTPLIDGVALHMKIRLITMGEGEGEYL 651  
 593 ESHDQALVADKTIAMVMDKMDYDPMALDRPSTPLIDGVALHMKIRLITMGEGEGEYL 652  
 652 EFGNNEGHEWIDPFRGDIHLPSGKFPVGNVSYDKCRRRDLGNSKHLRHYGQEOEQA 711  
 653 EFGNNEGHEWIDPFRGDIHLPSGKFPVGNVSYDKCRRRDLGNSKHLRHYGQEOEQA 712  
 712 IOHLEAVGFPMSEHGYISRKDERIRIIVFERGALVYFNFHMTSSYSDYRVGCLRGKY 771

DB 713 MOSLEKYGFMTHSDQYISRKHEEDKMIIFKGDVLFVFNHMSNSYEDYRVGCLRGKY 772  
 QY 772 KIVLSDPDLFGGFGRLSHDAHESFEGWYDNRDRSPVYTPCTFAVYALVE 824  
 DB 773 KIVLSDPDLFGGFGRLSHDAHESFEGWYDNRDRSPVYTPCTFAVYALVE 825  
 RESULT 11  
 101663  
 1.4-alpha-glucan branching enzyme (EC 2.4.1.18) 11b - maize  
 N:Alternate names: starch branching enzyme 11b  
 C:Species: Zea mays (maize)  
 C>Date: 19-Feb-1999 #sequence\_revision 19-Feb-1999 #text\_change 18-Jun-1999  
 R:Kin, K.N.; Fisher, D.K.; Gao, M.; Guiltinan, M.J.  
 Submitted to the EMBL Data Library, June 1998  
 A:Description: Molecular cloning and characterization of the amylose-extender gene en  
 A:Reference number: 214387  
 A:Accession: T01663  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Residues: 1-799 <KIM>  
 A:Cross-references: EMBL:AE072725; NID:q3511235; PIDN:AAC33764.1; PID:q3511236  
 A:Experimental source: strain B73  
 A:Genetics:  
 A:Gene: ae  
 A:Introns: 38/1; 86/3; 138/2; 171/2; 185/3; 205/3; 232/3; 271/3; 299/3; 340/2; 380/2;  
 C:Function:  
 A:Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha-  
 A:Pathway: glycogen/starch biosynthesis  
 C:Superfamily: 1.4-alpha-glucan branching enzyme  
 C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

Query Match Best Local Similarity 69.7%; Score 3169; DB 2; Length 799;  
 Matches 584; Conservative 84; Mismatches 93; Indels 68; Gaps 8;  
 2 GHYISGIRPCAPLCKSQSTGFHGRRTSSCLSFNFKAFRRVFGSKSHSDSNWVY 61  
 DB 33 GLFLTRARARGC-----SGTHGAMRAA-----AAARKA-----VM 62  
 QY 62 VTASKRVLPDGC---RIECYSSSTQDLEAPGVSESOV---LTVESTLIMDKIVEDEVN 115  
 DB 63 VPEGEN---DGLASRADSAQFOGDELEVP-DISEFTGAGAGVADQAL----- 106  
 QY 116 KESVPRREYISIKKSKRSRIPPRGGRITDIDPSLTGFQHLIDYRSQYKRLREID 175  
 DB 107 -----NKRVRVPPPDGDKIFQIDPMLQGYXYHLEYRYSLEVRRLRSDID 150  
 QY 176 KYBGSIDAEASRGYKRFGRSEGTITRYREMAPATGAALIGFNNWNNADVMONCGV 235  
 DB 151 EHBGGLAEASRGYKRFGRSEGTITRYREMAPATGAALIGFNNWNNADVMONCGV 210  
 QY 236 WEIIFELPNNDGSPPTPHGSRVRIKMDTPSGNKDSIPAMIKFSVQAPGLPYNGIYDPE 295  
 DB 211 WEIIFELPNNDGSPPTPHGSRVRIKMDTPSGNKDSIPAMIKFSVQAPGLPYNGIYDPE 270  
 QY 296 EEEKYVFNKQPKRPSLRITYESHVGMSSTPEYINTYANFRDYLPRIKKLGYNVQ 355  
 DB 271 EEEKYVFNKQPKRPSLRITYESHVGMSSTPEYINTYANFRDYLPRIKKLGYNVQ 330  
 QY 356 QEHSTYASFGYVNTFYAASSRFGTPDDLSLIDKAHGLGLVLMIVYHSHASTNTDGL 415  
 DB 331 QEHSTYASFGYVNTFYAASSRFGTPDDLSLIDKAHGLGLVLMIVYHSHASTNTDGL 390  
 QY 416 NMFDDGTHYFHSRGHMMWDSRLFYNGSWELRFLLSNARWMLDEYKDFGRDGV 475  
 DB 391 NMFDDGTHYFHSRGHMMWDSRLFYNGSWELRFLLSNARWMLDEYKDFGRDGV 450  
 QY 476 SMYTHHGLQVDFNTGNYEFGYATDVDAVYVLMILNDMIGLPEPEAVTTGDEDSGMPV 535  
 DB 451 SMYTHHGLQVDFNTGNYEFGYATDVDAVYVLMILNDMIGLPEPEAVTTGDEDSGMPV 510

QY 536 CIPVEDGVGFEDYRLHMAVADKWEIIOKREDEMKGDIYVHMLTNRRLKCKVSAESHD 595  
 Db 511 ALPHADGVGFEDYRLHMAVADKWEIIOKREDEMKGDIYVHMLTNRRLKCKVSAESHD 570  
 QY 596 QALVGDKTIAFWLMDKMDYDPMALDRPSTPLIDRGVALHMKIRLITMGIGEGYLTFMGN 655  
 Db 571 QALVGDKTIAFWLMDKMDYDPMALDRPSTPLIDRGVALHMKIRLITMGIGEGYLTFMGN 630  
 QY 656 EFGHEWIDPFRGDLHPSGKFPVGNNTSYDKCRRRFDLGSKHLRYHGMQEPDQAOIOL 715  
 Db 631 EFGHEWIDPFRGDLHPSGKFPVGNNTSYDKCRRRFDLGSKHLRYHGMQEPDQAOIOL 690  
 QY 716 EAVGPMTEHQYISRKDEDRITVEERGNLVEFNFHMTSSYSDRYGCLKPGKRYIVL 775  
 Db 691 EAVGPMTEHQYISRKDEDRITVEERGNLVEFNFHMTSSYSDRYGCLKPGKRYIVL 750  
 QY 776 DSDPLRGGRSLSHDAHESFEGWYDNRPSFVYTPCPTAVYALVE 824  
 Db 751 DSDPLRGGRSLSHDAHESFEGWYDNRPSFVYTPCPTAVYALVE 799

## RESULT 12

1.4-alpha-glucan branching enzyme (EC 2.4.1.18) II - maize  
 A:Accession: T02981  
 C:Species: Zea mays (maize)  
 C:Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 18-Jun-1999  
 R:fisher, D. K.; Boyer, C. D.; Hannah, L. C.  
 Plant Physiol. 102, 1045-1046, 1993  
 A:Title: Starch branching enzyme II from maize endosperm.  
 A:Reference number: 214808; MUID:94105320  
 A:Accession: T02981  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-799 <FIS>  
 A:Cross-references: EMBL:L08065; NID:q168482; PIDN:AA18571.1; PID:q168483  
 A:Experimental source: cultivar W64x182E  
 C:Function:  
 A:Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha-D-g  
 A:Pathway: glycogen/starch biosynthesis  
 C:Superfamily: 1,4-alpha-glucan branching enzyme  
 C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

Query Match 69.5%; Score 3160; DB 2; Length 799;  
 Best Local Similarity 70.3%; Pred. No. 4,4e-221;  
 Matches 583; Conservative 83; Mismatches 95; Indels 68; Gaps 8;

QY 2 GHYISGIRPCAPDLCKSGSTGFHGYRRTSSCLSFNKEAFSRVSGKSSHSDSNM 61  
 Db 33 GLFLTRGARVGC-----SGTHGAMRA-----AAAKA-----YA 62  
 QY 62 VTASKRVLPDG--RIECYSSSTDQLEAPCTVEESQV---LNDVESLMDKIVEDEVN 115  
 Db 63 VPEECN--DGLASRADSAQFQSDLEVP--DISEITCGAGVADALV----- 106  
 QY 116 KEVPMRETVSIRKIGSKPSIPPGRGORITDIPSLTGFROHLYRYOYKRLREID 175  
 Db 107 -----NKRVRPPPSDQKIFQIDPMLOGKHYHLERYSLYRIRISDID 150  
 QY 176 KYESGLDAFSGYKKEFGKSEGTITREMAFGATMAALIGDFNNMNDVMTONCGV 235  
 Db 151 EHEGGLAEFSHYERKFGNABEGITIREMAFGAFSAALVODVNMNDVMTONCGV 210  
 QY 236 WEIFLPNNDGSPPIPHGSRVKIRMDTPSGKSDISIPAMIKFSVOAPDELRYNGIYDPE 295  
 Db 211 WEIFLPNNDGSPPIPHGSRVKIRMDTPSGKSDISIPAMIKFSVOAPDELRYNGIYDPE 270  
 QY 296 EKVYFKNPQKRRKSLRIYSHYGMSTEPVINTYANREDDVLPRIKKIGYNVAVOLAI 355  
 Db 271 EKVYFKNPQKRRKSLRIYSHYGMSTEPVINTYANREDDVLPRIKKIGYNVAVOLAI 330

QY 356 QESHYASFGYHVTNFAASSRFGPDDLSLIDKAHELGLLVMDIYHSASTYTLNGL 415  
 Db 331 QESHYASFGYHVTNFAASSRFGPDDLSLIDKAHELGLLVMDIYHSASTYTLNGL 390  
 QY 416 NMDGSDTHGHVFSRPGHHMMDSRLFNTGSEVYLFLLSNARWMLDEKFGGFFDDVT 475  
 Db 391 NGPDGSDTHGHVFSRPGHHMMDSRLFNTGSEVYLFLLSNARWMLDEKFGGFFDDVT 450  
 QY 476 SMYTHHGLVDTFGVNYEFYADVDVAVYTLMLNDMIGLFPAYVIGEDVYGMPTV 535  
 Db 451 SMYTHHGLVDTFGVNYEFYADVDVAVYTLMLNDMIGLFPAYVIGEDVYGMPTV 510  
 QY 536 CIPVEDGVGFEDYRLHMAVADKWEIIOKREDEMKGDIYVHMLTNRRLKCKVSAESHD 595  
 Db 511 ALPHADGVGFEDYRLHMAVADKWEIIOKREDEMKGDIYVHMLTNRRLKCKVSAESHD 570  
 QY 596 QALVGDKTIAFWLMDKMDYDPMALDRPSTPLIDRGVALHMKIRLITMGIGEGYLTFMGN 655  
 Db 571 QALVGDKTIAFWLMDKMDYDPMALDRPSTPLIDRGVALHMKIRLITMGIGEGYLTFMGN 630  
 QY 656 EFGHEWIDPFRGDLHPSGKFPVGNNTSYDKCRRRFDLGSKHLRYHGMQEPDQAOIOL 715  
 Db 631 EFGHEWIDPFRGDLHPSGKFPVGNNTSYDKCRRRFDLGSKHLRYHGMQEPDQAOIOL 690  
 QY 716 EAVGPMTEHQYISRKDEDRITVEERGNLVEFNFHMTSSYSDRYGCLKPGKRYIVL 775  
 Db 691 EAVGPMTEHQYISRKDEDRITVEERGNLVEFNFHMTSSYSDRYGCLKPGKRYIVL 750  
 QY 776 DSDPLRGGRSLSHDAHESFEGWYDNRPSFVYTPCPTAVYALVE 824  
 Db 751 DSDPLRGGRSLSHDAHESFEGWYDNRPSFVYTPCPTAVYALVE 799

## RESULT 13

1.4-alpha-glucan branching enzyme (EC 2.4.1.18) I (clone sbe17) - potato (fragment)  
 A:Accession: T07824  
 C:Species: Solanum tuberosum (potato)  
 C:Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 21-Jul-2000  
 R:Khoshnoodi, J.; Blenow, A.; Ek, B.; Rask, L.; Larsson, H.  
 Eur. J. Biochem. 242, 148-155, 1996  
 A:Title: The multiple forms of starch branching enzyme I in Solanum tuberosum.  
 A:Reference number: 216155; MUID:97112484  
 A:Accession: T07824  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-830 <KH0>  
 A:Cross-references: EMBL:Y08786; NID:q1621011; PIDN:CAA70038.1; PID:q1621012  
 A:Experimental source: cv. Diamella; cell line Diamella  
 C:Genetics: sbe1  
 C:Function:  
 A:Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha-  
 A:Pathway: glycogen/starch biosynthesis  
 C:Superfamily: 1,4-alpha-glucan branching enzyme  
 C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

Query Match 48.0%; Score 2180; DB 2; Length 830;  
 Best Local Similarity 54.1%; Pred. No. 5.9e-150;  
 Matches 407; Conservative 116; Mismatches 177; Indels 52; Gaps 10;

QY 109 IVEDEVNKKSEVMRETVSIRKIGSKPSIPPGRGORITDIPSLTGFROHLYRYOYKRLREID 168  
 Db 1 VLTDD--NSTMAPLEEDYKTENIG-----LNDPRTLEPILDHFRIRMKRYV 45  
 QY 169 RLREEDKYEGSLDAFSGYKKEFGKSEGTITREMAFGATMAALIGDFNNMNDVMTONCGV 228  
 Db 46 DOKMLETEKEGLEEFQAQYLFKEFKREGGCLVIREMAFMAQAEVYIDDFNMGKSNHM 105  
 QY 229 TONECGWEIFLPNNDGSPPIPHGSRVKIRMDTPSGN--KDSIPAMIKFSVOAPDEL--P 285  
 Db 211 WEIFLPNNDGSPPIPHGSRVKIRMDTPSGN--KDSIPAMIKFSVOAPDEL--P 270

Db 106 EKDOFGVMSIRIP-DVDSKPVIPHNSRVKFKRKHGNGCWADRIIPAMIKYATADATKFAAP 164  
 QY 286 YNGIYDPEERKYYFKNDOPRPSLRILYESHVGMSTPEYINTYANERDDVLPRIKRL 345  
 Db 165 YGVGDVDPPEPRHFKYPRPRAPRIYEAHVGMSSSEPRVNSRERADVDPRITAN 224  
 QY 346 GYNAVOLMAIOHSHYASFGYHVTNFEYAAASSRFGPPDLKSLIDKAHELGLIYMDIVHS 405  
 Db 225 NNTVOLMAIMEHSHYASFGYHVTNFEYAAASSRFGPPDLKSLIDKAHELGLIYMDIVHS 284  
 QY 406 HASTVTLGLAMFD--GTGDHIFHSGRPHHMDSRLENFVNGSEVYRFLISNAKRMGLD 462  
 Db 285 HASNVNTOGLNFDIGGQSESYFLAERGYSIKLMDSRLENFVNGSEVYRFLISNAKRMGLD 344  
 QY 463 EKKDFGFRDGVTSMMYTHHGLVDFTGNYNFEYGYARDVAVVYIYMLNDMIGLPEEA 522  
 Db 345 EYNFGFRDGVTSMMYTHHGLVDFTGNYNFEYGYARDVAVVYIYMLNDMIGLPEEA 404  
 QY 523 VIGEDVSGMPTVCIPYEDGSGVGFYRLHMAVADKWEVILIO-KREDKMGDIYHMLTNR 581  
 Db 405 TYIADVSGMPTVCIPYEDGSGVGFYRLHMAVADKWEVILIO-KREDKMGDIYHMLTNR 464  
 QY 582 RMLEKCVASVASHDOALVGDKTIAFWLMDKMDYFMDLRSTPLIDRGVALHMKIRLIT 641  
 Db 465 RYTERCIAVASHDOALVGDKTIAFWLMDKMDYFMDLRSTPLIDRGVALHMKIRLIT 524  
 QY 642 MGLGEGEGLINMGNEFGEHPEWIDPRGDLHLPSCGFVPGNNYSYDKCRRRDLGNSKHLR 701  
 Db 525 MALGEGEGLINMGNEFGEHPEWIDPRGDLHLPSCGFVPGNNYSYDKCRRRDLGNSKHLR 573  
 QY 702 YHMOEFDOALHLEAYGFMTESEHOYISRKDERRIIVERGNLVYFVFNHMTSSYDY 761  
 Db 574 YKFNAPDRANNSLDEKSFSLASGKOIYSDMDONKVVFERGDLVYFVFNHMTSSYDY 633  
 QY 762 RVGLIKPGKRYKIVLSDDPLEGGFGRSLSHDAEHFSF-----EGWYDNRPSPFWYTP 813  
 Db 634 KYGCDLPCKRYKIVLSDDPLEGGFGRSLSHDAEHFSF-----EGWYDNRPSPFWYTP 693  
 QY 814 CRTAVVYALVEDE-----EVENLEPYA 835  
 Db 694 ARTCVAYYRDERMSETEYOTDICESELPFA 725

## RESULT 14

T06578  
 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) sbel precursor - wheat  
 N:Alternate names: starch branching enzyme I  
 C:Species: Triticum aestivum (common wheat)  
 C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 20-Jun-2000  
 C:Accession: T06578  
 R:Chibbar, R. N.  
 Submitted to the EMBL Data Library, April 1997  
 A:Reference number: Z15772  
 A:Accession: T06578  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-830 <CHI>  
 A:Cross-references: EMBL:Y12320; PIDN:CAA72987.1  
 A:Experimental source: cv. Fielder; kernels at 12 days post-anthesis  
 C:Genetics:  
 A:Gene: Sbel  
 C:Function:  
 A:Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha-D-g  
 C:Pathway: glycogen/starch biosynthesis  
 C:Superfamily: 1,4-alpha-glucan branching enzyme  
 C:Keywords: amyloplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltransf  
 F:1-61/Domain1: transit peptide (amyloplast) #status predicted <TNP>  
 F:62-830/Product: 1,4-alpha-glucan branching enzyme sbel #status predicted <MAT>

Query Match 47.6%; Score 2163; DB 2; Length 830;  
 Best Local Similarity 54.8%; Pred. No. 1e-18;  
 Matches 402; Conservative 115; Mismatches 175; Indels 42; Gaps 10;

QY 115 NKSEVPMREYTSIRKIGSKPR-----SIPPEGRQ-RITYDDPSLTGRHOLDTRYSOYKR 169  
 Db 56 SKFSVPV-----SAPRDYMTAAEDGVGLPYDDLPKPRAGKEHFYSRMKLYLD 105  
 QY 170 LREEDIDYEGSLDAPSRGKEFGFSRSEGTITTEYEMAPGATMAALIDFENMNPNDVMT 229  
 Db 106 QKSHLEKHGEGLEEFSGYGLKINTENDATVIRENAPPAAMDOLIDFENMNGSGHRMT 165  
 QY 230 QNEGVWEILFPLNADGSPPIPHGSRVKIRMDTPPSGN-KDISPAMIKFSVQABGL--PY 286  
 Db 166 KDNVGVMSIRI-SHVNGKPAIPHNSKVKFRFHKRDGLMVDVRVPAWILYAFDASKFGAPY 224  
 QY 287 NGIYDPEERKYYFKNDOPRPSLRILYESHVGMSTPEYINTYANERDDVLPRIKRL 346  
 Db 225 DGVIMDPSPSGERYFKPRPRAPRIYEAHVGMSSSEPRVNSRERADVDPRITAN 284  
 QY 347 YNAVOLMAIOHSHYASFGYHVTNFEYAAASSRFGPPDLKSLIDKAHELGLIYMDIVHS 406  
 Db 285 YNIVOLMAIMEHSHYASFGYHVTNFEYAAASSRFGPPDLKSLIDKAHELGLIYMDIVHS 344  
 QY 407 ASTNTLDGLAMFD--GTGDHIFHSGRPHHMDSRLENFVNGSEVYRFLISNAKRMGLD 463  
 Db 345 ASSKRTDGLNGYDVGOVNTQESYFHTGGRYHKLMDSRLENFVNGSEVYRFLISNAKRMGLD 404  
 QY 464 YKFDGFRDGVTSMMYTHHGLVDFTGNYNFEYGYARDVAVVYIYMLNDMIGLPEEA 523  
 Db 405 FMDGFRDGVTSMMYTHHGLVDFTGNYNFEYGYARDVAVVYIYMLNDMIGLPEEA 464  
 QY 524 TIEBDSVGMPTVCIPYEDGSGVGFYRLHMAVADKWEVILIO-KREDKMGDIYHMLTNR 582  
 Db 465 VVAEDVSGMPTVCIPYEDGSGVGFYRLHMAVADKWEVILIO-KREDKMGDIYHMLTNR 524  
 QY 583 WLEKCVASVASHDOALVGDKTIAFWLMDKMDYFMDLRSTPLIDRGVALHMKIRLIT 642  
 Db 525 YTERCIAVASHDOALVGDKTIAFWLMDKMDYFMDLRSTPLIDRGVALHMKIRLIT 584  
 QY 643 GLGEGEGLINMGNEFGEHPEWIDPRGDLHLPSCGFVPGNNYSYDKCRRRDLGNSKHLR 702  
 Db 585 ALGGDGYLINMGNEFGEHPEWIDPRGDLHLPSCGFVPGNNYSYDKCRRRDLGNSKHLR 633  
 QY 703 HGMQEFDOALHLEAYGFMTESEHOYISRKDERRIIVERGNLVYFVFNHMTSSYDY 762  
 Db 634 KYMNAFDQAMNMLDDEKSFSLSSKQIYSDMDONKVVFERGDLVYFVFNHMTSSYDY 693  
 QY 763 VGCLKPGKRYKIVLSDDPLEGGFGRSLSHDAEHFSF-----EGWYDNRPSPFWYTP 814  
 Db 694 VGCCLPCKRYKIVLSDDPLEGGFGRSLSHDAEHFSF-----EGWYDNRPSPFWYTP 693  
 QY 815 RTAVVYALVEDEVE 828  
 Db 754 RTCVAYYRVEEKAE 767

## RESULT 15

S34730  
 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) precursor, amyloplast - potato  
 N:Alternate names: starch branching enzyme  
 C:Species: Solanum tuberosum (potato)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 07-Dec-1999  
 C:Accession: S34730; S38733; S18594  
 R:Poulsten, P.  
 Submitted to the EMBL Data Library, December 1992  
 A:Description: Starch-branching enzyme cDNA from Solanum tuberosum.  
 A:Reference number: S34730  
 A:Accession: S34730  
 A:Molecule type: mRNA  
 A:Residues: 1-861 <POD>  
 A:Cross-references: EMBL:X69805; NID:9396080; PIDN:CAA49463.1; PID:9396081  
 R:Khoshnoodi, J.; Ek, B.; Rask, L.; Larsson, H.  
 FEBS Lett. 332, 132-138, 1993  
 A:Title: Characterization of the 97 and 103 kDa forms of starch branching enzyme from  
 A:Reference number: S38732; M01D:94009663

A:Accession: S38733  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 76-95;236-244, 'X', 246-255;311-329;393-402;515-520;523-529;545-558; 'F', 636-64  
 A:Accession: S38732  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 318-492, 'S', 494-538, 'K', 540-550 <KHM>  
 R:Kossmann, J.; Vliesser, R.G.F.; Mueller-Roeber, B.; Willmitzer, L.; Sonnwald, U.  
 Mol. Gen. Genet. 230, 39-44, 1991  
 A:Title: Cloning and expression analysis of a potato cDNA that encodes branching enzyme;  
 A:Reference number: S18594; MUID:92079917  
 A:Accession: S18594  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 279-527 <KOS>  
 C:Genetics:  
 A:Gene: SBE  
 A:Genome: nuclear  
 C:Function:  
 A:Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha-D-g  
 A:Pathway: glycogen/starch biosynthesis  
 A:Note: final step in biosynthesis of glycogen or amylopectin  
 C:Superfamily: 1,4-alpha-glucan branching enzyme  
 C:Keywords: amyloplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltransf  
 F;1-75/Domain: transit peptide (amyloplast) #status predicted <TNP>  
 F;76-861/Product: 1,4-alpha-glucan branching enzyme #status experimental <MAT>

Query Match 47.2% Score 2145; DB 1; Length 861;  
 Best Local Similarity 51.6% Pred. No. 2,2e-147;  
 Matches 411; Conservative 116; Mismatches 183; Indels 86; Gaps 12;  
 QY 34 LSFNEK-----EATSRKPFSGKSSH-----ESDSNMVYASKR 67  
 DB 1 MEINFKVLSKPIRGSPFSPKSVSGASRKIKTFPSOHSGLKFGSOERSWDSITPKSR 60  
 QY 68 VLPDGRTECYSSSTDLAEAGTVSESOYLTVESLIMDKIYEDVKNKESYPMRETVSI 127  
 DB 61 VRDERK-HSSAI-----SAVLTD-----DNSTMAPLEEDVKT 93  
 QY 128 RKIGSKPRSIIPPGRCGRIVYDPSLTGFRQHLDIRYSQYKRLREIDIKESGLAFSRG 187  
 DB 94 ENIG-----LNLDPTEPLYDHRFRHRRKRYVDQKMLEKEGLEEPAQS 139  
 QY 188 YEKFGFSRSEGTITRYEMAPGATWALIGDPNMNPADVYQNECGWEIFLPNNAQS 247  
 DB 140 YLKFGRNEDGCIYRMAAPAOEDEVIQDPNGMNGSNHMEKDOFGVWSIRIP-DVDSK 198  
 QY 248 PPIPHGSRVKIRMDTPSGN-KDSIPAMIKFSVOAPGEL--PYNGIYYDPPEEKYVFKNP 304  
 DB 199 PVIHNSRVKFRFGHGVVWDRIPIAWIKYATADATKFAAPYDGVVWDPSPSRERHKKYP 258  
 QY 305 QPKPKSLRIYESHVGSSTPEVINTYANFRDVLPRIKKLGYNVOLAIOEHSYYASF 364  
 DB 259 RPKPRAPRIYEAHVGSSEPRVNSYREFADVLPRIKANNYVOLAIMEHSYYGSF 318  
 QY 365 GYHTNTYPAASRRGTDDLSLIDKAHELGLVLMDIVSHASTNTLDGLNMFDD--GT 421  
 DB 319 GYHTNFPFVASSRKGNEPDLKYLIDKAHSLGLQVLYDVVSHASNNVTDGLNGFDIGGS 378  
 QY 422 DGHYFHSGRGHMMWDSRLFNYSGEVLRFLSNARWMLDEYKDFGRFDGVTSMYTH 481  
 DB 379 QESYFHAERGYHKLMDSRLEFVNAMVELRFLSNLKWMLLEYNFDFGRFDGITSMLYH 438  
 QY 482 HGLQVDFGTNNEYFGYATDVAVVYLMMLNDMTIHLPEAVTIGEDVSGMPTVCIYED 541  
 DB 439 HGINNGFTGNNEYFSEATDVAVVYLMMLNHNKIFPDATVLAEDVSGMPLGPRVSE 498  
 QY 542 GGVGFDYRLHNAVADKWEIIQ-KREDEMKMGDIYHMLITNRWLEKCVSYAESHDQALVG 600  
 DB 499 GGIGFDYRLAMAIIDPKWIDYIKKNRNEDEWMSKEVTSLSLTNRRTYKCIAYAESHDQSIYV 558

QY 601 DKTIAFWIMDKMYDFMALDRPSTPLIDRGVALHKMIRITMGLSGEGLTNMGNEFGHP 660  
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 QY 661 EWIDFPRGDHLPSGKFPVGNNSYDKCRRRFDLGNKHLRYHGMQEPDQAIQHLLEAVG 720  
 DB 619 EWIDFPR-----EGNNMSYDKCRROWMLADSEHLRYKFNNAFPRANNS-JDEKFS 667  
 QY 721 FMTSEHGYISRKDERDRIYFEGNLTVEFNFHWTSSYSYDVRGCLKPKYKTYVJSDDP 780  
 DB 668 FLASGRQIVSSMDDDNKVVVEFERGDLVFNFPKNTYEGYKVCDDLPGKYRYVAJSDAM 727  
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 DB 728 EFGCHGRTHGDVDFHT 743

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